Run on:

em_ov:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length DB
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                                                                     November 1, 2001, 20:37:40 ; Search time 33971.2 Seconds (without alignments) 12140.628 Million cell updates/sec
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1 tatcaggtgactgaattcta......ttcgccaagtcttttgaca 26664
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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em_htgo_inv:*
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AC005277
AF304371S2
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Description

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SUMMARIES

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| G60268 SHGC-130964 G58081 SHGC-104094 AF0308694 Gorilla g AX608570 Sequence AC02314 Homo sapi AC010458 Homo sapi AC010458 Homo sapi AC010519 Homo sapi AC01054 Homo sapi AC01054 Homo sapi AC012329 Homo sapi AC01311 Homo sapi AC013664 Homo sapi AC013681 Homo sapi AC018644 Homo sapi AC018944 Homo sapi AC018844 Homo sapi AC018844 Homo sapi AC018924 Homo sapi AC018927 Homo sapi AC018944 Homo sapi AC018927 Homo sapi | | 11 Homo 12 Homo 13 Homo 14 Homo 17 Homo 18 Homo 19 Homo 10 Homo 10 Homo 11 Homo 11 Homo 12 Homo 13 Homo 14 Homo 16 Homo 17 Homo 18 Homo 19 Homo 10 Homo 10 Homo 11 Homo 11 Homo 12 Homo 13 Homo 14 Homo 15 Homo 16 Homo 17 Homo 17 Homo 18 |
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                                            Submitted (23-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 23, 1998 this sequence version replaced gi:3335015.
All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                       Only the first 118.8 kilobases of this clone are being submitted. The remainder overlaps accession number AC005274 (WICGR project L350).
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| Д | 79633 | TIGGGGGCTTAAGTGGTGAGTATATTCTTTGCAGTGTCAGGGCTGGTGGGAAGTCTCTG 79692 | ć | | |
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| δλ | 2041 | | δλ | 312 | aatctt |
| QQ | 79693 | GGATTTTAACCGGCTTTACCATTTTTCCAAGTCTGGGGTGGGCAGCTACTTTTTTTT | qq | 80773 | |
| οy | 2101 | ttttttttttgtcagtggcgtgatcttggctcactgcaacctttgccttctgggctcag 2160 | oy Oy | 3181 | cctccag CCTCCAG |
| qq | 79753 | | ò | 3241 | |
| Oy Dp | 2161 | gtgatccctcacctcagcctcccaaatagctggaccacactgtgccccatcacacct 2220 | 7 원 | 80893 | |
| ογ | 2221 | ggctaattttttttgtatgttttgtagcgacggggttttgctatgttgcccaggctggtc 2280 | Οy | 330 | tataaga |
| QQ | 79873 | | <u>අ</u> ර | 80953 | |
| OY D | 2281 | tcaaacttctgcgatcctcctgtctcggcctcccagagtgctgggattacaggcatgagc 2340 | P G | 3361 81013 | taaagca TAAAGCA |
| 07 | 2341 | caccgcacctggcctggaattcttttataccagcccagtcagcagcagcagcacagacatt 2 | Oy | 3421 | gcagett |
| QQ | 79993 | | 셤 : | 81073 | |
| Qy Db | 2401 | aaaagctgtgactcaggagaacagattttaatatggataccacctcttaagtgttaccat 2460 | δ q | 3461 | racacte racacte |
| Qy Ph | 2461 | coacttagtttettgcgttgcggggacagagtttgtggcagtaaactggagagtctagc 2520 | Oy Ob | 3541 | agaagaa AGAAGAA |
| δ | 2521 | digity that the control of the contr | QY | 360 | tttgtct |
| qq | 80173 | AGTGGTGATTACAGTTAATATGTTTACCGCAGACGCCATTGGCACTTGGCAGCCACACA 80232 | a à | 3661 | |
| δγ Op | 2581 80233 | catacccactgtccagattaccctgtcatttatgtctatcaaccggaaggtcaggattgt 2640 | à q | 81313 | |
| oy P | 2641 | gttgcagccaaattgtgtgggcttggtggcatggaccggaaggagtgaagtgtagacca 2700 | Qy Qu | 3721 81373 | ttcaaga TTCAAGA |
| à g | 2701 | State Stat | QY | 3781 81433 | gcaatac GCAATAC |
| δλ | 2761 | atgattocttacattttgcacactgggtgccttgctgcttcaccctagtgacagctcagc 2820 | QY | 3841 | acacttc |
| Op | 80413 | | ò | 3901 | |
| Oy Dp | 2821 | ccattctagaggcatttaaagaatatttggtgtctgttacacctctagctggcatcactt 2880 | qq | · D | |
| Qy | 2881 | ctgctctgtacatcttccctggttgtacttccaaagctggaaggtggagatgtagataaa 2940 | Oy Dp | 3961 81613 | tgctgcc GCTGCC |
| Š i | 2941 | tagttggattagtacggggtgctcctctgttagtgacgacaggtcaaattgatgagaga 3000 | VQ QD | 4021 | tgcctct GCCTCT |
| a : | 80593 | TAGITGCATTAGTACGGGGGGGCTCCTCTGTTAGTGACGACGGGTCAAATTGATGAGGGA, 80 | QY | 4081 | 01- |
| D C | 80653 | ccgattiratgarccittiaggargarccitacittaaaggaaaccgggcticcaa 3060 | qa , | 81733 | |
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| Οy | 3121 | tctttccttttgtaatatcagtaacaagaattttcctttttgcaaatcagtctttctg |
|--------------|----------|--|
| qa | 80773 | |
| ΟŸ | 18. | 40 |
| Q | 83 | CTCCAGAGATACCTGGTCGTTGAAACGCTTCCCCTTTCAAGTTAAAAAGACTTGAGTTC 808 |
| ۶ ج | 3241 | tgattaactatgtgaccttgatcaagttactttacctttctgagctttagttattatcatc 3300 |
| 2 6 | ה ל ס | GALIAACIAIGACCIIGAICAAGIIACIIIIACCIIICIGAGCIIIAAGIIIAAIC 0033 |
| 중 점 | 80953 | cacaagargaacaacacacacagagreyreyraaagarcaaagagagagacaca 3300 |
| QY | | aaagcactaaatcactttattagatatatgtttggcaccaagtaggcacacaagaaagg 34 |
| qq | 81013 | - |
| δλ | 3421 | tttgtttttattcaataaatttctgacatcttcttacctttcagtccagcttat 34 |
| qq | | CAGCTITIGITITIATICAATAAATITCIGACATCTICTTACCTITCAGICCAGCTTAT 81 |
| 0 | 3481 | actcttgagaaggcgtgtgtgtgttgaatataacagttcattt |
| Q | 81133 | ACACTCTTGAGAAGGCGTGTGTGTTGTTGAATATAACAGTTCATTTTCCAGTCCTTA 811 |
| QY | 3541 | aagtcaccaagacctgttaagtctttccccaaaataacgtttgaaatccatcc |
| QQ | 81193 | GAAGAAAGTCACCAAGACCTGTTAAGTCTTTCCCCAAAATAACGTTTGAAATCCATCC |
| Qγ | 09 | tgtctcttattgaggccttccttatttctgttttctatgcctgtaaactacaatagc 3660 |
| QQ | 81253 | TIGICICITATIGAGGCCTICCTTATITCTGTTTTCTATGCCTGTAAACTACAATAGCC 813 |
| Qy | 3661 | ccatattcattctcgccttcctgtaatccatctgccacacagcagccagaggtcac 372 |
| q | 81313 | cccaratrcarrescerrecrararecarerecaeaecaecaeaeaeaeaee 813 |
| οy | 3721 | gaaaagtagtgtcacttgccaccctaaagcccttcatgggctcccatt 378 |
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| οy | 3781 | ◂ |
| qq | 81433 | CAATACAATCAAAACACCTTGATATGGCCTACAAGTCCTGTAGGCCCCGGCCGCTACC |
| Qy | 3841 | catctgtacccatcgctgaactgcagctgcatgggctgactcttatgt |
| qq | 81493 | TTTCCATCTGTACCCATCGCTGAACTGCATGCCATGGCTGACTCTTATGTCCCT |
| Qy | 3901 | taactccctggccacttcaggactttcgcccttccgcgggttccctctgcctcttctaat 3960 |
| qq | 81553 | AACTCCCTGGCCACTTCAGGACTTTCGCCCTTCCGCGGTTCCCTCTGCCTCTTCTAAT 816 |
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| QQ | 9 | GCCTCTTCTTCTCTAGACAAGTIGGATCCCAGCCTTCTGTATTTTTCATTTTCCTTGCA 81 |
| ΟŊ | 4081 | taatgccactaagctgtttctgttatcgtgtttccttttgtctcctc 414 |
| QQ | 81733 | AGCACTTAGCATAATGCCACTAAGGTGTTTCTGTTATCGTGTTTCCTTTTGTCTCCTCC 817 |
| δy | 4141 | actggcctgattagagcaaggcctccatctttttcctgctatatccttggcatctgat 4200 |
| QQ | 81793 | SGCCTGATTAGAGCCAAGGCCTCCATCTCTTTTCCTGCTATATCCTTGGCATCTG |

| | 5401 caaaatacacttttatttatttctaaaaatggtaatctccttagaaagtctggttttcg | 5461 tgtcagattcccaccataattctgaggcaattcagttgctcgtggttggt | 5521 ttactcttccaccatcttcactattgcatcactttgctgttgtgyggttttcttgta | | 5641 cccatacacagtgagtatgaaagccaggtttcccaggaggagggtgtacgtcctgagtaa 57 | 5701 agaaacatgatgaaatagaactgaacacttgctgtgggcaccctgtttgtgttct | Oy 5761 gagcatgattagaaaatttagttgaggaatgaagaatatggctcctgccctggcttataaa 5820 | Qy 5821 cttacggatgtctgacttatgcctaatgatagtgattatgctttggaatattagataatc 5880 | Qy 5881 aagcactgttggtaaatagattgcattcaagtttgcacattcatt | | Qy 6001 ttttttaaataaataatgattacagcaacctaaaagaagtgttgttgggggttagaagct 6060 | Oy 6061 cctgcaaattccgaagtatcagggccagatgatgtggtcttagcttaggaaaagagttag 6120 | Oy 6121 tettgteettgaaettggetaaagacatteatgtetggttttaettacatgtgaagagg 6180 | taccaagcagtagggtatttccttgttagtactaatgtgatgatgcttactaagtagt | Oy 6241 gctgatgggtgacagaccagagcaccagcaaggccagagaagtccagaacctggcgag 6300 | Qy 6301 gagatgaggcttacactgactgaaggcagaaggcagcaggaggaggaggaatgtgccgga 6360 | Oy 6361 gcaatggcacaagtgctctaggccagtgctgtgatgagctgatcagcactcccattgcc 6420 |
|--|---|--|---|---|--|---|--|---|---|---|---|---|--|--|---|---|--|
| 4201 ataatggatactcagtaaatatttgtaataaatgatgttcaaaatatttactaagct | ATACCTATIGGTAACCTITTAAATACTIGAATAGTIGCT ataactgctcattctttttttcattaggaaaata | 4381 caaaatatttctggtccattgaaaggaatagaactgggtacgtctttgtctgtgactca Hillillillillillillillillillillillillill | Qy 4441 tcctctgctatttctaacttatatatgccctgacctctcaaattagaatccattaaaaac 4500 | Qy 4501 atcaacatcaaaccaaatcaaatgcttcatcaccacgagatttttttt | Qy 4561 ttttttggatagagtcttgcttaccaggctggagtgcagtggcatgatctcggctc 4620 De 82213 TTTTTGGATAGAGTCTTGCTTTCTTACCAGGCTGGAGTGCCATGATCTCGGCTC 82272 | Qy 4621 actgcaacctccacctctgggttcaagccattctcccacctcagcctctgggtagcta 4680 Db 111111111111111111111111111111111111 | Qy 4681 ggactacaggcgcatgccatcaggtcaattttttgtatttttagtagagcgggg 4740 | gccaggatagtctcgatctcttgaccttgtgatctgccgcctcagc | tttctgt | Oy 4861 gttcccacctcatgctgtaaaaataggggccaggtcggcaggagtgattgaacagctgat 4920 | attctccatccagacgcaggctcctgct | 1 ttccagaggtgcttctcgttcgttgagttgctttgagttgggggggg | aggtttgtggccaactttgtacattgaaacgcagctccagctgcgcagggggg | tgggaagagcctcactgaggatgctagtaggagctcttgtcctgg 516 | Oy 5161 cactggtgtgtatctgtggcttgttaatactcctttttatagaaacactaatacttgt 5220 | 5221 ttcaaaatatacatcagctcttctggtttgcgatgataggttccctggcttcactattct | 5281 gtttgttaactt&ggtctctgaaagttgagtactagtttcttgtttttcaattttaacg |

| 4013 | CAATGGCACAAGTGCTCCTAGGCCAGTGCTGTGATGAGCTGATCAGCACTCCCATTG 99cttgctcctcctgctcaqatqccttctctcacctqacccctqctqtaqccaccc |
|------------|---|
| 73 | 41 |
| 33 | gcctgagttgcatccacctgtttgttgtccatttccagcaccctgttcttcgctccatgg 6540 |
| 541 | catgtgacagttaactttcatatgtgatttgcgtgatcgatgttaacatgctcagttttg 6600 |
| 193 | |
| 601 253 | ccgatcactgttttttcagtgtccagcggcctcagtgagtg |
| 661 | ttgcagctgtgctttagcttcttagagcagcgaatttttttcccttgatcttgagcctta 6720 |
| 313 | |
| 721 | actaaatgtaaaatgaggctccttcttgagataggtaccctttgggtctatgtgtttag 6780 |
| 373 | |
| 781 | cgggagtgatgataataaataagcatgtctacaacccacatgctgtttagataacacgtt 6840 |
| 433 | |
| 841 | gttgagttggtactgtggccgaggctgtgagctaagcagaaacataaacattaataggac 6900 |
| 493 | |
| 901 | ataggigcagcccagaaaccaggiaggaagitaactaactagtiatitcciacigitatag 6960 |
| 553 | |
| 961 | taaaaggtgtgctgatttaattggcgttctggcattcccatgtatgaacgtctgggcctt 7020 |
| 613 | |
| 021 | ggctgtcagctcaccttgtgcagtgtgtaatttggtggtatctgtactgaccaggtgaac 7080 |
| 673 | |
| 081 | agaggagggaaagcaccaaccatggcagagtccagaaaggcctctcagcaggctcagtc 7140 |
| 733 | |
| 141 | cagagogatetteagaetecgagtygaatgaaaatgageeacaeteeacatggtaata 7200 |
| 793 | |
| 201 | gtataaacaaaacagagcagcagaaaggcttgcgttttcttaattctctgccttgtaatg 7260 |
| 853 | |
| 261 | cttgtagagagtcattattgtaagaaagccaggtgtgtaaacagatccttcttcctgggc 7320 |
| 913 | |
| 321 | ttactataacttggcccgttggggaatgagaagggttgttgtaaaggtggcagcctgca 7380 |
| 973 | |
| 381 | actttaataatgaccagtccacagttttggccaccagggtctgggtaggcccaaaactg 7440 |
| 033 | |
| 441 | tgttctgttttcccagaggaacagggctgacaaacggattcattttgtatttttcat 7500 |
| 093 | |

| a 7560 | A 852 | 9 7620 85272 | t 7680 | T 85: | t 7740 | 85 | rt 7800 | co -⊟- | t 7 | r 855 | 7 | Ŋ | t 7 | T 856 | π – 90 | r 85692 | ra 8100 | A 85752 | t 8160 | I 858 | c 822 | ထ - ပ | 19 8280 | G 859 | 9 8340 | rg 85992 | 9 840 | တ | ag 8460 | ص دن | 852 | т 86172 | ga 8580 | - |
|--|---------|--|---|---------|--|--|--|--|---|--|---|---|--|--|--|--|---|---|---|---|--|---|---|--|--|--|---|--|---|---|---|---|--|---|
| acatttatqcaaattttccattaatqtqqaaactataactqctaaqccaatq | | caaatcagtgagaggctctgcacgtcttccagaatgacagcccactgggaaac; | tecaagatgagatgtagetcaggagteaggeegettegggagtttgttg | | tggcaaagctcggcagctcctcttctgtcctgaggtct | AGAAGGTCAGCGTTGGCAAAGCTCGGCAGCTCCTTTCTGTCCTGAGGTCT | tgactgagaacaggctgaccctatgtgctgtccttgtttggatggcaccggg | GACTGAGAACAGGCTGACCCCTATGTGTGTGTGTGTTTGGATGGCACCGG | gacaccagcatttctctgcaggcctttgaacttttgtgttatttcatatat | TTCTCTGCAGGCCTTTGAACTTTTGTGTTATTTCATATAT | ttataaagcacattacaatatatttttctctgtcttctccagtcctaggtg | AAAGCACATTACAATATATTTTTCTCTGTTTTCTCCAGTCCTAGGTG | oatttaaaaaaatttcacttgccattctaaagtttttctggtgagagttttg | CATTTAAAAAAATTTCACTTGCCATTCTAAAGTTTTTCTGGTGAGAGTTTTG | catttacgcaaacacatctccacataagtagggaaaaaagtcttcttgagta | CATITACGCAAACACAICICCACAIAAGIAGGGAAAAAAAAGICITCIIGAGIA | gtcttcagcctttgtattgggacagtagcgtccattaatttttatgtgaagtg | GTCTTCAGCCTTTGTATTGGGACAGTAGCGTCCATTAATTTTTATGTGAAGTG | gtatcgggtcataatcagtctgtgatgtcttcacagctttcacatttaccttg | GTATCGGGTCATAATCAGTCTGTGATGTCTTCACAGCTTTCACATTTACCTTG | caagtgtgttttcctcaggtgttagccagagaagaggggtcagggactcttc | AAGTGTGTTTTTCCTCAGGTGTTAGCCAGAAGAAGAGGGGTCAGGGACTCTTC | gtagctttcatctgtaaggtaaggaagactttccggagggctgtacatgactg | ractitcatcigiaaggiaaggaagactitccggaggcigiacaigacig | ggtcagcgacctctggtttgcacttttcattaatttgagggtaggcactct. | GTCAGCGACCTCTGGTTTGCACTTTTCATTTTGAGGGTAGGCACTCCT | gagacaagaagatagcagatcttcagaaaagctgatggaaggccgggtgca | gagacagagaragcagarcticagaaagcigatggaaggccgggtgca | acgcctgtaatcccagcactttgggagtccaaggcaggtggatcacgaggtca | <u> ACGCCTGTAATCCCAGCACTTTGGGAGTCCAAGGCAGGTGGATCACGAGGTCA</u> | gagaacagcctgaccaacgtggtgaaaccctgtctgtactaaaaatacaaaat | GAGAACAGCCTGACCAACGTGGTGAAACCCTGTCTGTACTAAAATAC | ggtgtggtggcgcatgcctgtaatcccagctacttgagaggccaaggcaaga | |
| aatqt | TAATGTA | gacagtc | tt (| GAGTTAA | ccttaac | TTAA | tag | CTAG | Jac | AAAGACT | tatgt | ATATGTG | atgtgtc | TGTGT | gttttc | TTTT | attagtg | TTAGT | aattagg | rtag | gataatc | TAAT | ctggtcg | SGTC | ggtcttg | GTCTT | ttacctg | PACCT | tggctca | GGCTC | gagtttg | AGTTT | tagctgg | = |
| 7501 | 85153 | 7561 | 762 | C) | 7681 | 85333 | 7741 | | 7801 | 85453 | 7861 | 85513 | 7921 | 85573 | 7981 | 85633 | 8041 | 85693 | 8101 | 85753 | 8161 | 85813 | 8221 | 85873 | 28 | 85933 | 8341 | 85993 | 8401 | 86053 | 8461 | 86113 | | |
| ò | . A | yo d | ò | Db | οy | qq | Qy | QQ | δy | Dp | δy | qq | Qy | qq | δŽ | Dp | οy | QQ | ΟÝ | qq | QY | qq | ΟŊ | qq | δy | В | ογ | QQ | Qy | οp | Qγ | Dp | δy | |

ø

ctcagcctcccgtgtagctgggatcacaggtgcctgccaccatgcccg 10800 tgccttggcctccaaagtgctggattacaggcgtgagccatcatg atttatattgtctgatttttaaactgttttctatggtaatctttaaa geagttgccctattatcaggcagccgttcctgggggctgccagctgc rttetggeteteateagtetteeagataetetgeatteeteagagagg tttttttttttgagacagagtctcgctctgtcaccaggctggagt gagtagetgggactacaggagcgcaccaccatgcccagctaatttttg AGTAGCTGGGACTACAGGAGCGCACCACCATGCCCAGCTAATTTTTG

| QQ | 88393 | GTGATTCCTTGCCTCAGCCTCCCGTGTAGCTGGGATCACAGGTGCCTGCC | ż | 1001 | 1 1 1 1 |
|----------|------------|--|----------------|-------|----------------------------------|
| δλ | 10801 | gctaatttttgtattgttagtagacacaggtttcgccatgttggccaggctagtctcga 10860 | i i | 89533 | GCTAATTT |
| qq | 88453 | GCTAATTTTGTATTGTTAGTAGACACAGGGTTTCGCCATGTT | ò | 6 | atotocta |
| Oy | 10861 | actectgaecteaagtgatetgeetteeteageeteetaaagtgetgggttaeaggagt 10920 | q _Q | S | ATCTCCTG |
| 3 8 | 3. 8 | COC - - - - - - - - - | Οy | 12001 | agccgctg |
| g g | 88573 | gaaccaccaysccasycciticaartacciticaticaticaticaticitii 1990 | qq | 89623 | AGCCGCTG |
| δŏ | 860 | agacggagtctttctgtgttgcccaggctggagtgcggtggcgcaatcttagctcactgc 1104 | ζ Q | 12061 | tgacatta TGACATTA |
| QQ | 88633 | | δò | 12121 | gttageet |
| oy D | 11041 | aacetcetcetecaggeteaagtgatteteatgeateagetteeegagtagetgggaet 11100 | , do | 89773 | |
| ογ | 11101 | tcaggtgccgccacacacttggctaattttgtgtttttagtagagacggggtttcac 111 | 0y | 218 | tgttagge |
| QQ | 88753 | TCAGGTGCCGCCACCACTTGGCTAATTTTTTTTTTTAGTAGAGGGGGTTTCAC 88812 | <u>a</u> : | 12241 | TGTTAGGC |
| کې دو | 11161 | catgitggccaggctggtcttgaatttctgacctcaaatgatcctcctgcttcagcctcc 11220 | S 8 | 989 | AACAGTGT |
| 3 (| 1000 | CATOLICACCERGOLICATORALITICACCACARATORALCCACCACCACCACCACCACCACCACACACACACACAC | ογ | 12301 | μ. |
| y d | 11221 | Gaaagtgctgggattacaggcgtgagccactgccccaacagcaagtaccttttaaacat | qq | 89953 | TTTTATTA |
| δ | 128 | tagagacatttagttgccatcctcaaacccgtttgggtgtgtggagagaatgttgggtcg 1134 | Οy | | gcttttag |
| Ob | 88933 | | අ . | 90013 | GCTTTTAG |
| δy | 11341 | tgacatggttgttagttatctaaagatgtcagccatcaatca | δ 5 | 242 | aaagcaat |
| qq | 88993 | | àà | 12481 | AAAGCAA |
| à i | 11401 | actgaagctgtaatccttcatctaggatgatattttttaagatggaaattctacaaccc 1146 | 5 A | 90133 | TTTTTTG |
| 2 | _ | ACTGAAGCTGTAATCCTTCATCTAGGATGATTTTTTTAAGATGGAAAATTCTACAACCC 891 | οy | 12541 | gctcacto |
| oy ob | 1146189113 | tgagaataaggatttcaggtccaaatttgagactcagcctacgagtaactcttaactt 11520 | qq | 90193 | GCTCACTG |
| Qy | 11521 | cagagagttaaaagaagatgcacagttgatgaagatttaaaggagaaaatggaaatcaaa 1158 | QY | 6 | ctgggatt |
| QQ | 89173 | | අ | 0 1 | CTGGGATT |
| οy | 11581 | | à d | 90313 | 91111111 |
| QQ | 89233 | | ò | | agectee |
| ر ا | 11641 | ttttttttttcctataaaatgattgtgaagttttctggtagaattattgtttgcctttcta 1170 mminmynmynchnin naasaanan menenaastatttctggtagaattattgtttgcctttcta 1170 mminmynmynmynchnin naasaanan menenaasta menenamen naasaanan menenamen naasaanan naasaan | 7 A | _ | AGCCTCCG |
| 3 8 | 09690 | IIIIIIIICCIAIAAAAIGAIIGIGAAGIIIIICIGGIAGAAIIAIIGIIIGCCITICIA 8933 | ٥y | 12781 | tttttt |
| g 5 | 89353 | algraatagaatattagggttttttttttttttttttttggaacagagtctca 11760 | qq | 90433 | TTTTTT |
| ò | 7 | etetategeccaggetggaatgeagtageacatetegagteactgeagteteeecte 1182 | δy | 12841 | agccccta |
| 연 | 89413 | | d0 : | 90493 | CCCCT |
| Qy Dp | 11821 | ctgggttcctgcctcagcctccgagtagctgggactacaggcgcacgtcaccacacccg 11880 | S A | 90553 | CTTGGTGC |
| | | | | | |

| Qy Dp | 11881 89533 | gctaatttttgtatttttagtagtgacagggattcaccgtcttagccagggtggtcttg 11 | 1940 |
|----------|----------------|---|-------|
| Oy Db | 11941 89593 | atctcctgacctcatgatctaccgcctcggcttcccaaagtgctgggattacaggcatg 1. | 2000 |
| Oy | 12001 | agccgctgtgcctggctattagggatttttattataatttatctccaagataaaagcag 1; | 12060 |
| Dp | 89653 | | |
| Qy | 12061 89713 | tgacattatattgccacataattgaaaaatacaagagaaataaaaatcatccatgcttt 1; | |
| Qy | 12121 | gttagcctatcactgtcattgaaatattatgttacatggcagtttgcttgc | 218 |
| Db | 89773 | | 983 |
| QY | 12181 | tgttaggcaacgctctggtgacattcctttagctattaattgaggaatgtagaatgacag 1: | 12240 |
| Dp | 89833 | | |
| Qy Dp | 12241 89893 | aacagtgtttctcctcaatgatacttgaaggatatttatt | 230 |
| Qy | 12301 | ttttattaaatttataatgagttaatgctgggaaataaaacactgatttaatcattttg 1: | 236 |
| Db | 89953 | | 001 |
| oy D | 12361 | gottttagtactaaagcatttgacaataaatgacttcttcagaatatggtataccttctg 1; | 2420 |
| Qy | 12421 | gaattgtaaggaaacaacatcattttatttttatttt 1: | 248 |
| Dp | 90073 | | 013 |
| Q Q | 12481 | agtgcaatggcgcgatctcg 1 | 254 |
| | 90133 | | 019 |
| oy | 12541 | ctcactgcaacatccgcctctggttcaagcgattctcctgcctcagcttcctgagttg 1. | 260 |
| B | 90193 | | |
| Qy | 12601 | ctgggattacaggcacgtgccaccacgcctggccaatttgtatttttagtagagacggg 1: | 266 |
| Dp | 90253 | | |
| Qy | 12661 90313 | ggtcaggctggtctcaaactctgacctcaggtgatctgccgcctc 1: | 272 |
| oy | 12721 | octccgaaagtactggaattacaggcgtgagccaccgtgcctggccaacattatt 1 | 278 |
| G | 90373 | | |
| Qy | 12781 | aaatacacttctaagaaattgattaaaaccaaccttcttcatt 1: | 284 |
| Db | 90433 | | 049 |
| Qy | 12841 | agococotaagatoacatotatgttototttgttgcagottoacttaaagagaggaaactt 1: | 12900 |
| Db | 90493 | | |
| Qy | 12901 90553 | cttggtgctcaaagcaaaggagatgggcctcccagtgtgagtgtggggggtaaggcttct 1; | 2960 |

| 92832 15240 92892 15300 92952 15360 | 15420 93072 15480 93132 15540 93192 | 325 566 331 572 337 578 | 93432 15840 93492 15900 93552 15960 | 16020 93672 16080 93732 16140 93792 16200 93852 16260 |
|--|--|--|--|---|
| TGCCGTGAGCAGCCTGTGAGAGCATGGCCTGGGGGGGGGG | cagcagtagatagagaggtatagagcccagccagcgcacttagggtaactcttctg [| | SCCACTTICTEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | ctocatggoctgctotctgotgtctttcattcctcagggtttgggtccctatttgt [|
| 773 181 833 241 893 301 | 15361 93013 15421 93073 15481 93133 | 7 3 6 2 6 7 | ש נו ש נו ש נו ש | 15961 93613 16021 16081 93733 16141 93793 16201 |
| 00 OO OO OO | OA DB OA OB OA OB OA OB OB< | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 90 00 00 00 | |

| ò | 16261 | at ctatttottcacaggtttgggcctgacacccaggacttggtcctgaatgagaactgt | 16320 |
|----------------|-------|--|-------|
| | 91 | 99-0-29 ***COLOR OF STATE OF S | 97 |
| Qy | 16321 | cctcagttcacaacttcgcagccacaagattcaaacccagctcaacctcatccaccg | 16380 |
| qa | 93973 | GCCTCAGTTCACAACCTTCGCAGCACAAGATTCAAACCCAGGCTCAACCTCATCCACCGG | 94032 |
| Qy | 16381 | gacatcttcccctgctcaccagtttccgctgtaaggtagtgtctcagacyggcccttg | 16440 |
| qq | 94033 | ACATCTTCCCCCTGCTCACCAGTTTCCGCTGTAAGGTAGTGTCTCAGAACCGGCCCTTG | 94092 |
| QY | 16441 | cggcccagctctcgtccctctttctctccatgaatgtg | 0 |
| qa | 94093 | GGCCCAGCTCTCCTCTTTCTCTCCATGAATGTGTTTTGTCTCTTTCAGAA | 415 |
| Οŷ | 16501 | caccetcagtgtgcccatggttcagggtgaatgcctcctcaagtaccagctc | 16560 |
| οgα | 94153 | AGGCCCCACCTCAGTGTGCCCATGGTTCAGGTGAATGCCTCCTCAAGTACCAGCTC | 421 |
| QY | 16561 | cgtcccaggaggagtggcagaggtctgtgccatcttgaactaatggaatcgtctcagtc | 16620 |
| qq | 94213 | GTCCCAGGAGGAGTGGCAGAGGTCTGTGCATCTTGAACTAATGGAATCGTCTCAGT | 94272 |
| QY | 16621 | tctgtaaatagccacatagtaaatgtt | 16680 |
| QQ | 94273 | AGTIGGGAAACATITICTGTAAATAGCCACATAGTAAATGTTCCAGGAGGCTCTCCAGA | 433 |
| ογ | 16681 | atatggtctctgttgtaactattcaactccgctttgagcacaaaagaaacacggac | 674 |
| ପ୍ | 94333 | | 94392 |
| οy | 16741 | ttgg | 80 |
| Db | 94393 | GCTAATGAATGGGCTTGGCTGTGTGCCAGCGTGAATTTATTAGAAAAGCAGCCTACT | 94452 |
| 0y | 16801 | tttccaaaattgcctt | 96 |
| QQ | 94453 | CAGGCTGGGTTGGGGCGGATTGGGGCCAGTAGTTCTCCTTTTCCAAAATTGCCTT | 451 |
| QY | 16861 | gcatgggaatagcagtgatagagctcgtgtgtttcacagtatagaaaataggaaatgtgt | 16920 |
| q _Q | 94513 | CATGGGAATAGCAGTGATAGAGCTCGTGTTTCACAGTATAGAAAATAGGAAATGTG | 94572 |
| Qy | 16921 | gatgaacaaagtcacccataatcctgttgcccagagataatgattgat | 16980 |
| qq | 94573 | ATGAACAAAGTCACCCATAATCCTGTTGCCCAGAGATAATGATTGAT | 94632 |
| QY | 16981 | ttcttgatttgtgtatgtgggtttatattgtcagtcttttcctgtatcactaaacagtct | 17040 |
| qq | 94633 | TCTTGATTTGTGTATGTGGGTTTATATTGTCAGTCTTTTCCTGTATCACTAAACAGTC | 94692 |
| Οy | 17041 | taagtaacaagattttattgtattccaaatagggatgtttactcatttgggatgtttc | 17100 |
| qa | 94693 | AAGTAACAAGATTTTTTTTTTGGTATTCCAAATAGGGATGTTTACTCATTTGGGATGTTT | 94752 |
| Qγ | 17101 | aatttttgttgtttttaatgaatgaatgaacaataaatgtcttatatata | 17160 |
| qа | 94753 | | 94812 |
| QY | 17161 | ggaactctgttcccttcaagtcattcctaaatgtgggattactggcccagagtgtgagac | 17220 |
| qa | 94813 | GAACTCTGTTCCCTTCAAGTCATTCCTAAATGTGGGGATTACTGGCCCAGAGTGTGAGA | 94872 |
| QY | 17221 | ttgttaaggtacttgataaatgtaagatgccatcttgaaagcctcttccagtacaatcca | 17280 |
| qq | 94873 | TGTTAAGGTACTTGATAAATGTAAGATGCCATCTTGAAAGCCTCTTCCAGTACAATCCA | 94932 |
| . 0y | 17281 | accaggaaagtgaacagccttactgcccacatctttattttaattaa | 17340 |
| qa | 94933 | CAGGAAAGTGAACAGCCTTACTGCCCCCACATCTTTTTTTAATTAA | 94992 |

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| 1 cacca | CACC | | | H 6 | 3 5 | 1 ttca | - E | 3 - | 3 1 | 3 1 | - A - B | | н е | 1 aggta 3 AGGTA | 1 gtgg GTGG | - | TTCC | 1 aactg 3 |
|---|--|--|---|---|--|--|---|--|--|---|--------------------------------|---|--|---|--|---|---|--|
| 2064 | 0 0 | 2 10 | 11 | 4 7 | 9 9 | 9859 | 9865 | - i | 7 5 | m m | 2124 | 2130. | 2136 | 07 | 148 913 | 2154 | بنتمق | 2166 9931 |
| δλ | qa , | g G | da G | Oy Dp | Oy Dp | y da | Oy Dp | QY Dp | Oy Dp | QY | Oy Op | Qy Dp | Qy Db | oy D | oy D | Qy Dp | go Go | oy o |
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| 97212 | 27 | 19680 97332 | 19740 97392 | 19800 | 19860 97512 | 19920 97572 | 19980 97632 | 20040 | 20100 97752 | 20160 97812 | 20220 | 20280 | 20340 | 20400 | 20460 98112 | 20520 98172 | 20580 | 20640 98292 |
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| GCGACC | AAATP | caatt | atago | tgcca IIIII | tgtgt | attta | gette secric | gaegg | ccatt | agccac | aaccg | aaacca NAACCA | tttca | aacago | statge | tccto | gacto | otttac |
| GGAGGAT | TOTA | tacac | gacag | 399995 11111 399995 | tagte | aggtgt AGGTG1 | tgaad stgaad | cgtgaa GTGAA | acaaat \CAAA | tcca2 | tecca CCCA | cacte | ggatte 3GATT | cttgga | ataage ATAAG | caaaa AAAA | catgte | gcaaac CAAAC |
| GCTGG | goacacacus con constanta a da | aagaat \AGAAT | tttggt TTGG1 | Egccag GCCAC | ctgtct | aaaaga AAAAGA | ttcca | gtggcagaggagcgcaagtaggaagtggacgcttgtgaagacgg | Egggaa FGGGA | Egcago TGCAGO | 209001 - - - | aatgad AATGAG | ctgcatgctggctcacttttgacccaaaggaatggattgtttcacat. | tette | tcaac CAAC | ttaaad TAAAG | cttgt crrGr | cagta AGTA |
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| a: + | ת) — ני | aagaaa AAGAA | agaat AGAAT | gcgaa GCGAA | ggata GGATA | atgtg | gagaa SAGAA | gcaga SCAGA | tggct rGGCT | tetec | tagcc AGCC | Eccac FCCAC | catgc ATGC | aaaag AAAAG | atteg ATTCG | cttcc | tgaaa TGAAA | gtggc GTGGC |
| GGA | GCA | ycata? CATA | actgga ACTGG | + - F | aagcto AGCTO | agaata AGAATA | gggct - | acgtg | Sacto | Egcag GCAG | rtecetgt | acgtt ACGTT | ggctg GCTG | cagag AGAG | tgaag GAAG | gcatco | cgatt GATT | ggago GAGO |
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| 97153 (| 213 | 19621 1 | 19681 a | 19741 o | 19801 0 | 19861 a | 19921 | 19981 | 20041 6 | 20101 6 | 20161 | 20221 | 20281 0 | 20341 | 20401 | 20461 | 20521 | 20581 |
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| q | 100453 | GAGAGAGGGCTGCAGACCCTAACCCGGAGGGGATGGCCTGGGGCCTGGCTGACGCATGT 1 | 100512 |
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| GIGATITGGAAGAGGTAAGGGGCACAGGGGGAAGGGGGGAAGGGGGCACAGGCCGGGAAGGGGGG |
| |

| ò | 25021 | gcagcacaacgtcccaagccatcagcgtggggatgcggatgaacgcggagttcattat | 25080 |
|--------|--------|--|--------|
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| đ | 103333 | GGCCTGTTGGCTTGTGGCCAAGGAGGGCCGTTGGCCGCTGTGTGTG | 33 |
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| qq | 10 | SCCTGTTTGTTGCGCGACATCGAGGAGATGGAGGAGCGCAGGGAGAAGCGGGAGAGCTG | |
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| ΟŸ | 26041 | gatctgggagaccctgaactcagaaggctgtgtgtcttctgcccacgcacg | 26100 |
| Q | 103693 | TEGGAGACCCTGAACTCAGAAGGCTGTGTGTCTTCTGCCCCACGCACG | 103752 |

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Snyder S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A., M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.

Direct Submission
Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt Lake City, UT 84108, USA
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/db_xref="G1:10880931"
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Reid, J.E.,
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[ (bases 1 to 740)
Tavtigian,S.V., Simard,J., Teng,D.H.F., Baumgard,M., Beck,A., Camp,N.J., Carillo,A.R., Chen,Y., Dayananth,P., Desrochers,M., Dumont,M., Farnham,J.M., Frank,D., Trye,C., Chaffari,S., Leavitt,A., Leblanc,G., McArthur-Morrison,J., Pederson,R.T., Reid,J.E., Richards,S., Schroeder,M., Smith,R., Snyder,S.C., Swedlund,B., Swensen,J., Thomas,A., Tranchant,M., and Cannon-Albright,L.A.
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                                                                                                                                                                                                                                                                                                       tctgccctccttgctggtagaagctgaagaacacggtcccccaagaaggcagctcaagata
                 103753 TCTGCCCTCCTTGCTGGTAGAAGCTGAAGAGCACGGTCCCCCAGGAGGCAGCCCAGGATA
                                                             ggtggtatggagctgtgccgaggcttgggctcccacataagcactagtctatagatgcct
                                                                                                                        cttaggactggtgcctggcacagccgcgggccaggaggctgccacacggaagcaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84108, USA
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                                                             /protein_id="AAG24439.1"
/db_xref="G1:10880930"
/translation="EQRRGKHQPWGSPERPLSRLSPERSSDSESNENEPHLPH"
143 c 184 g 193 t
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Homo sapiens putative prostate cancer susceptibility protein
HPC2/ELAC2 gene, exon 7 and partial cds.
AF304371.1 GI:10880000
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/Product="putative prostate cancer susceptibility
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<301. .>420
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/db_xref="taxon:9606"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2908)
Tavtigian,S.V., Simard,J., Teng,D.H.F., Abtin,V., Baumgard,M.,
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                                                 gtaatgettgtagagagteattattgtaagaaageeaggtgtgtaaacagateettette
                                                                                                                                                    7015 ggccttggctgtcagctcaccttgtgcagtgtgtaatttggtggtatctgtactgaccag
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                         0; Mismatches
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1. .2908
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/product="putative prostate cancer susceptibility protein
HPC2/ELAC2"
                        Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Illaev, D., Janecki, T., Kort, E.N., Lalty, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A. A candidate prostate cancer susceptibility gene at chromosome 17p 11175785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25810 aggtctgcttttggagactttccaacaatgcccaagctgattccccactgaaagccctgt 25869
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Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P.,
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100.0%; Pred. No. 0;
ive 0; Mismatches 0; Indels 0
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/db_xref="GI:10880933"
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/db_xref="taxon:9606"
/chromosome="17"
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Matches 657; Conservative
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Clone distribution: MGC clone distribution information can be found through the I.M.AG.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 9 Rown i Column: 17.

Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2997)
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Submitted (29-JAN-2001) National Institutes of Health, Mammalian
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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BC001939
BC001939.1 GI:12804972
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2552 CTTGCTGGTAGAAGCTGAAGAGCACGGTCCCCCAGGAGGCAGCTCAGGATAGGTGGTATG
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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Mon Nov

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://lmage.llnl.gov Series: IRAL Plate: 2 Row: c Column: 13.

Location/Qualifiers
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/protein_id="AAH04158.1"
/db_xref="G1:13278771"
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KRGPSGCSGGPNTVYLQVVAAGSRDSGAALYVFSEFNRYLFNCGGGVQRLMQEHKLKV
ARLDNIFLTRMHWSNVGGLSGMILTLKETGLPKCVLSGPPQLEKYLEAIKIFSGPLKG
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DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERAL
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ISSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTWPCEALVRMGKDATL
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EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSRE
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Greene, Mark Ketteman and Anuradha Madan
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-MAR.2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
           26350 tecagcaaagtgattecetgeacaccagagacaagcagagtaacaggatecagtgggteta 26409
                                                2852 TCCAGCAAAGTGATTCCCTGCACACACAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTA 2911
                                                                                                                                                                                                                                                                                                                                                                                                     BC004158 3006 bp mRNA PRI 16-MAR-2001
Homo sapiens, putative prostate cancer susceptibility protein,
clone MGC:2441, mRNA, complete cds.
                                                                                                                                                     26410 agtgtccgagacttaacgaaaatagtatttcagctgcaataaagattgagtttgcaa 26466
                                                                                                                                                                                           2912 AGTGTCCGAGACTTAACGAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTGCAA 2968
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
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/db_xref="Locusin:60528"
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/clone="MGC:244Pe="Lung, small cell carcinoma"
/clone_lib="NTF_MGC_7"
/lab_host="DHIOB-R"
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Contact: Robert Strausberg, Ph.D.
TTB: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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BC004158.1 GI:13278770
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EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLISRE
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                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative prostate cancer susceptibility protein"
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Pred. No. 0;
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Submitted (27-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84103, USA
Location/Qualifiers
                                                                        Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E., Lablanc, G., McArthur-Worrison, J., Leavitt, A., Leblanc, G., McArthur-Worrison, J., Pederson, A., Penn, B., Peterson, R.T., Reid, J.E., Richards, S. Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
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              Neuhausen,S., Rommens,J. and Cannon-Albright,L.A.
A candidate prostate cancer susceptibility gene at chromosome 17p
Nat. Genet. 27 (2), 172-180 (2001)
Tranchant, M., Woodland, A.M., Labrie, F., Skolnick, M.H.,
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Pred. No. 1.2e-172;
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1. .2481
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Best Local Similarity 99.1%;
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                                                        JOURNAL
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Tavtigian, S. V., Simard, J., Teng, D.H.F., Abtin, V., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffaris, S., Gupte, J.S., Hu, R., Illev, D., Janeck, T., Kort, E.N., Leaty, K.E., Leavitt, A., Lebhanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                             gaccetgaacteagaaggetgtgtgtettetgeceeaegeaegeaecegtatetgeeete
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                                                                                                                                                                                                               2321 AGGICTGCTTTGGAGACTTTCCAACAATGCCCAAGCTGATTCCCCCACTGAAAGCCCTGT
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LAGGLEDGEPQQKRAHTEEPQAKKVRAQ"
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Pan troglodytes ELAC2 mRNA, complete
AF308698
                                                                                            Score 606; DB
Pred. No. 0;
0; Mismatches
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                    858 9
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                                                                                            Query Match 2.3%;
Best Local Similarity 99.8%;
Matches 656; Conservative
                    808 c
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/pocedi_id="BAA91666.1"
/db_xref="G1:7022622"
/db_xref="G1:7022622"
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                               /clone="NT2RP2000985"
/clone="lib="NT2RP2"
/note="cloning vector: pWE18SFL3; mRNA from NT2 neuronal
precursor colls after 2-weeks retinoic acid (RA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 429)
Olivier,M. and Cox, D.R.
Unpublished, Olivier, M., Cox, D.R. (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G60268 429 bp DNA STS 30-MAR-2000
SHGC-130964 Human Homo sapiens STS genomic, sequence tagged site.
G60268
G60268.1 GI:6125437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1016 cgctgcggcacctgcgcacgcgagagaagcgcggaccgtcggggtgtcccggcgacaa
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100.0%; Pred. No. 1.4e-167;
iive 0; Mismatches 0;
                                                                                                                                                                                                      75. .2639
/note="unnamed protein product"
      /cell_type="teratocarcinoma"
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Matches 321; Conservative
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4 (SIL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                              26191 toccacataagcactagtctatagatgcctcttaggactggtgcctggcacagccgcggg 26250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aagaagtettggaaacagacggcgcacettteetetaatecagcaaagtgatteeetge 26370
                                                                                                                                                                                                                                 26131 gcacggtcccccaggaggcagctcaggataggtggtatggagctgtgccgaggcttgggc 26190
                                                                                                                                    2513 TGTGTCTTCTGCCCCACGCACGCACCCGTATCTGCCCTCCTTGCTGGTAGAAGCTGAAGA 2572
                                                                                                                                                                                                                                                                        2753 AAGAAGGCTTGGAAACAGACGCAGCACCTTTCCTCTAATCCAGCAAAGTGATTCCCTGC 2812
2813 ACACCAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCGAGACTTAACGAAA 2872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-FEB-2000
                                                                                                    tgtgtcttctgccccacgcacgcacccgtatctgccctccttgctggtagaagctgaaga
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Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mRNA,
clone_lib:NT2RP2 clone:NT2RP2000985.
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/db_xref="taxon:9606"
/cell_line="NT2"
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VERSION
KEYWORDS
SOURCE
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TITLE
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                  G58081 220 bp DNA STS 30-MAR-2000 SHGC-104094 Human Homo sapiens STS genomic, sequence tagged site. G58081. G1:6123400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ends sequenced at TIGR from the RPCI11 BAC library. Designed developed at the Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy 15459 ccagcgctacctacccttctgcacctgcctaaactttctgtgggattcctgccttcccag 15518
                           117 TAATCCAGCAAAGTGATTCCCTGCACACCAGAGACAAGCAGAGTAACAGGATCAGTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 minutes
30 seconds
30 seconds
23 seconds
                                                                                                                                                                                                                                                                                                                                 Stanford Human Genome Center Stanford Human Genome Center Stanford University School of Medicine 4005 Miranda Ave. '2nd Fl., Palo Alto, CA 94025, USA Tel: (650) 320-5800 Fax: (650) 320-5801 Email: olivier@shgo.stanford.edu Primer A: CTTRATGGAATCCTCAACCAAACG Primer B: CTGCACCTGCCTAAACTTTCTGT STS size: 191 PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 220;
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each 200 uM
0.07 units/ul
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94 degrees C for 30
60 degrees C for 30
72 degrees C for 23
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Perkin Elmer 9700
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Best Local Similarity 100.0%; Pred. No. 1.7e-105;
Matches 210; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                  1 (bases 1 to 220)
Olivier,M. and Cox,D.R.
Unpublished, Olivier, M., Cox, D.R. (2000)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                       Contact: Michael Olivier, David R. Cox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46
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Total Vol:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="17"
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67 g
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8.3
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2. .192
2. .24
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KEYWORDS
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seconds
seconds
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                        Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5801
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: TTTGCTGGATTAGAGGAAAGGTG
Primer B: AGTGAAGATCTGGAGACCCTGAA
STS size: 322
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 429;
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94 degrees C for 30 sc
60 degrees C for 30 sc
72 degrees C for 23 sc
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Perkin Elmer 9700
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each 1 uM
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Pred. No. 4.4e-125;
0; Mismatches 1;
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Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="17"
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115 c 108 g
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Denaturation:
Annealing:
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Best Local Similarity 99.5%;
Matches 415; Conservative (
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106. .128
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RS Tavtigian,S.V., Simard,J., Teng,D.H.F., Baungard,M., Beck,A., Camp,N.J., Carillo,A.R., Chen,Y., Dayananth,P., Desrochers,M., Dumont,M., Farnham,M., Frank,D., Frye,C., Ghaffari,S., Gupte,J.S., Hu,R., Iliev,D., Janecki,T., Kort,E.N., Laity,K.E., Leavitt,A., Leblanc,G., McArthur-Morrison,J., Pederson,A., Penn,B., Peterson,K.T., Reid,J.E., Richards,S., Schroeder,M., Smith,R., Snyder,S.C., Swedlund,B., Swensen,J., Thomas,A., Tranchant,M., and Cannon-Albright,L.A. Gorilla gorilla ortholog of human HPC2/ELAC2

I Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      User gorilla gorilla

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Buaryota; Metazoa; Chordata; Catarrhini; Hominidae; Gorilla.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

1 (bases 1 to 2893)

Tavtigian,S.V., Simard,J., Teng,D.H.F., Abtin,V., Baumgard,M.,

Beck,A., Camp,N.J., Carillo,A.R., Chen,Y., Dayananth,P.,

Cantigian,S., Gupte,J.S., Hu,R., Iliev,D., Janechi,T., Kort,E.N.,

Laity,K.E., Leavitt,A., Leblanc,G., McArthur-Morrison,J.,

Schroeder,M., Smith,R., Snyder,S.C., Swedlund,B., Swensen,J.,

Thomas,A., Tranchant,M., Woodland,A.M., Labrie,F., Skolnick,M.H.,

Neuhausen,S., Rommens,J. and Cannon-Albright,L.A.

A candidate prostate cancer susceptibility gene at chromosome 17p

1117785
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Submitted (27-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84103, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Tavtigian, S.V., Carillo, A.R., Chen, Y., Dayanarth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Shetzson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J., and Cannon-Albright, L.A.
                                                             15579 agtgtccacacgattccatttattttacaccctccacactcttcagggtgtctgaacaaa 15638
210 CCAGCGCTACCTACCTTCTGCACCTGCCTAAACTTTCTGTGGGGATTCCTGCCTTCCCAG 151
                                                                                                                                                                                    90 AGTGTCCACACGATTCCATTTTTTTTTTACACCCTCCACACTCTTCAGGGTGTCTGAACAAA 31
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Gorilla gorilla ELAC2 (ELAC2) mRNA, complete cds.
AF308694 GI:10946488
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/organism="Gorilla gorilla"
/db_xref="taxon:9593"
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                                                                                                                                                                                                                                                                          /gene="ELAC2"
1. .2481
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AUTHORS
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/db_xref="GI:10946489"
/translation="WAALGSLIRAAGRTMSQGRTISQAPARRERPRKDPLRHLRTRE
/translation="WAALGSLIRAAGRTMSQGRTISQAPARRERPRKDPLRHLRTRE
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VRLDNIFLTRHHWSNVGGLSGMILTLKETGLPKCVLSGPPQLEKYLEAIKIFSSGPLKG
IELAVRHGAPETBETTWYVOIPTHSEDRRGKHQPWOSPERPLSKLSPRESSDSESN
ENEPHLPHGVSGRRGVRDSSLLVVAFICKLHLKRGNFLVLAKEMGLPVGTAAIAPIIA
AVROCKSITHEGRELLAFELCTPPDPGAAFVVVCPDESFIQPICENATFORYGKAD
APVALVVHMAPESVLVDSRYQWMERFGPDTQHLVLNENCASVHNLRSHKIQTOLNLI
HPDIFFDLISFPCKREGPTLSYPRWOGECLLKYQLRRFREWQNDAITCNPREFTVBA
LQLDNFQQSVGETRSYQVDYPAPAREKSOYPEITELGTGSA-PMKIRNVSATLVNISP
DTSLLLDCGEGTFGOLCRHYCDQVDRVLGTLAAVFVSHLHADHHTGLINILLQREQAL
ASIGKPLHFLLVVAPSQLKMLQOYHNQCOEVLHHTSMIPARCALLNRGKDATL
ISSLLRTCDLEEFQTCLVRHCKHAFGCALLWHTSGWRVVYSGDTMPCCALURKKGNDATL
LIHBATLEDGLEERANFERTHSTTSGAISVGRRMNABFILLNINFSQRYAKVPLFSPNFN
EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMERRRERRERRERRERRERRENGMAALLSGE
LAGGLEGDFPQQKRAHTEEFQARKVVARQ"

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Enamalia; Euthberia; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 386)

S Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.,

Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.,

Lamson, G., Drmanac, R., Crkenjakov, R., Drmanac, S., Dickson, M.,

Lamson, G., Drmanac, R., Kita, D., Garcia, V. and Strache-Crain, B.

Human genes and gene expression products

Human genes and gene expression products

CHIRON CORPORATION (US); HYSEQ, INC. (US)

Location/Qualifiers
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/note="similar to Homo sapiens HPC2/ELAC2"
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/db_xref="taxon:9606"
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2 (bases 1 to 151889)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
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HOMO sapiens chromosome 17 clone RP11-42F20 map 17, *** SEQUENCING AC008158
AC008158
                                                                                                                                                                                                                                                                                                      Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-42F20
                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 105787)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (04-OCT-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Oct 4, 2000 this sequence version replaced gi:7711447. Draft Sequence Produced by DOE Joint Genome Institute
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Homo saplens chromosome 19 clone CTD-2265M8, complete sequence.
ACC10458
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DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
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100.0%; Pred. No. 3.2e-32;
Live 0; Mismatches 0; Indels 0;
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/db_xref="taxon:9606"
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DOE Joint Genome Institute.
Direct Submission
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AC008158.12 GI:13123374
HTG; HTGS_PHASE1.
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                                                                    AC010458.5 GI:10567845
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AC008158/c
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Submitted (08-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 53108, USA
Waterston, R.H.
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                                                                                                                                                              MO 63108, USA
On Dec 22, 2000 this sequence version replaced gi:8569878.
Center project name: H_NH0266008.
Location/Qualifiers
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Homo sapiens clone RP11-26608, complete sequence.
ACO23114
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. 9.4e-33;
thes 0;
                                                                    0.6%; Score 158; DB 10;
100.0%; Pred. No. 2.7e-76;
iive 0; Mismatches 0;
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35094 c 38389 g 47103
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Waterston, R.H.
                                                                                   Best Local Similarity 100.
Matches 158; Conservative
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                   Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dearr, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Maldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Ragner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M., New, X., Wagner, A., Direct, Subnission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-JUL-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Feb 25, 2001 This sequence Version replaced 91:11181825. All repeats were identified using RepeatMasKer: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
Beckerly, R., Benn, J., Brown, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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76100 76199; gap of 100 bp
76200 88646; contig of 12447 bp in length
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130499 151889: contig of 21391 bp in length
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Best Local Similarity 100.0%; Pred, No. 3.4e-32
Matches 80; Conservative 0; Mismatches 0
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/db_xref="taxon:9606"
/chromosome="17"
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Center clone name: 42_F_20
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1. .151889
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JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 221507)

Williams, S.

Direct Submission

L Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Chone requests: clonerequest@sanger.ac.uk

On Jun 7, 1999 this sequence version replaced gi:4688873.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Emm., EMBL: Sw., SWISSPROT; Tr., TREMBL: Wp., WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22
HS407F11 221507 bp DNA PRI 12-DEC-1999
Human DNA sequence from clone CTA-407F11 on chromosome 22q12
Contains ADRBK2 gene for adrenergic beta receptor kinase 2, the
YESP (v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1)
pseudogene, ESTs, a ca repeat polymorphism, genomic marker D228421,
STSS, GSSs and two putative CpG Islands, complete sequence.
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Location/Qualifiers
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/note="LIME repeat: matches 5460. .5757 of consensus"
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1213. .1293
/note="MLTIA1 repeat: matches 1. .89 of consensus"
1294. .1594
                                                                                                                                                                                                                                                                                                                                         HTG; ADRBK2; adrenergic; ca epeat polymorphism; CpG island; D228421; receptor kinase; YESP.
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/note="MIR repeat: matches 52.
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/db_xref="taxon:9606"
/chromosome="22"
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                                                                                                                                                                                                                                                                                                                     AL022329.9 GI:5002625
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/note="22 col
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repeat_region

Qy 12695 ctgacctcaggtgatctgcc 12714

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2511. 3278
//note="11PAl0 repeat: matches 5367. .6165 of consensus" 3280. 3345
//note="MLTHF repeat: matches 474. .568 of consensus" 3397. 3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8156. .8466
//octe="Allox repeat: matches 1. .311 of consensus"
8467 .8381
//octe="Milk repeat: matches 123. .262 of consensus"
8688 .8737
//octe="L2 repeat: matches 2700. .2749 of consensus"
8873. .8966
//octe="L2 repeat: matches 2020. .2113 of consensus"
9063. .9385
//octe="L2 repeat: matches 2030. .2303 of consensus"
9101. .9585
//octe="Milk repeat: matches 2030. .2303 of consensus"
11072. .11169
                                                                                                                                                                                                                                                                                                      4598. 4781
Anote="MERZ1B repeat: matches 598. .790 of consensus"
6622. 6159
Anote="L2 repeat: matches 2107. .2747 of consensus"
                                                                                                                                                                                                                          3744. .4326
/note="MBR21B repeat: matches 32. .598 of consensus"
                                                 of consensus"
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13293. .13545
                                                                                                                                                                                                                                                               4327. 4597
/note="%luJb repeat: matches 9. .281 of consensus"
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                                                                                                                                                                                     397. 3709 note="AluJo repeat: matches 1. 312 of consensus"
                                                                 2014. .2497
/note="MLT1E repeat: matches 1. .519 of consensus"
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note="AluSx repeat: matches 1. .312 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of consensus"
'note="AluY repeat: matches 1. .301 of consensus" 595. .1918
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complement(11107. .11644)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 8. .123 of consensus"
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/hote="MIR repeat: matches 6. .253 of consensus"
11670. .12192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        copies 2 mer ca 100 conserved"
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                                               89.
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11693. 12092
//note="match: GSS: Em:B14426"
12336. 12380
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2983. .13292
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                                               /note="MLT1A1 repeat: matches
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/note="match: STS: Em:Z23711"
                                                                                                                                                                                                                                                                                                                                                                                    6815. 7105
/note="match: STS: Em:L02019
natch: STS: Em:L02019"
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/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(14742. 14990)
/note="match: GSS: Em:AQ1
15262. 16143
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/note="MIR re
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/note="L2 re
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/note="26
                          repeat_region
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155/3. 15603

//note="Single clone region"

15684. 15687

//note="wingle clone region"

15688. 15719

//note="weed data"

1010 (15726. 15895,55119. 55195,95334. 95407,

1011 (15726. 15895,15179. 125270,129558. 129657,

135912. 135990,138279. 138479,140931. 141025,

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146897. 146956,15222. 154318,154851. 154951,

166987. 169123,172026. 172139,173031. 174689)

//gene="match: cDNAs: Em:M73216 Em:M87855 Em:X69117

Em:M44019 Em:M87845 Em:M73216 Em:M87855 Em:X69117

Em:AA215794 Em:AA223716 Em:AA312780 Em:AA250907

Em:AA25940 Em:AA897081 Em:AA312780 Em:AA250905

Em:AA27956 Em:AA897081 Em:AA312780 Em:AA250905

Em:AA287692 Em:AA897081 Em:AA279133 Em:AA250907

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Em:AA27685 Em:AA4047782 Em:AA279445 Em:R63891 Em:AA32870

Em:AA057617 Em:AA047782 Em:AA27944 Em:R63891 Em:AA32870

Em:AA057617 Em:R80858 Em:AA5735 Em:R63890 Em:AA32897

Em:T29185 Em:R07780 Em:Z45735 Em:C16726 Em:AA322997
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/product="bK407F11.2 (adrenergic, beta, receptor kinase
2)
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/product="bK407F11.2 (adrenergic, beta, receptor kinase
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112318. .112419,114372. .114446,118481. .118542,
123038. .123089,125179. .125270,129558. .129657,
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166840. .160706,161810. .161905,165150. .165312,
168987. .169123,172026. .172139,173031. .174689)
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100.0%; Pred. No. 3.6e-32;
Live 0; Mismatches 0; Indels 0;
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/codon_start=1
               29 copies 3 mer gga 77
.15725
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                                                                                /note="100 copies 2 mer gg
15573. .15603
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HTG 12-SEP-2000 DNA HTG 12-SEP-2000 Arbono sapiens chromosome 8 clone CTB-482E7 map 8q13, WORKING DRAFT SEQUENCE, 12 unordered pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 24703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 others
             f unknown length
y of 930 bp in length
f unknown length
y of 1211 bp in length
woknown length
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gap of unknown length
22291: contig of 823 bp in length
gap of unknown length
23295: contig of 1004 bp in length
gap of unknown length
                                                                            of 408 bp in length
                                                                                                                                                                                 of 764 bp in length
unknown length
                                                                                                                                                                                                                                                           contig of 775 bp in length
gap of unknown length
contig of 764 bp in length
gap of unknown length
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gap of unknown length
contig of 833 bp in length
gap of unknown length
                                                                                          unknown length
of 820 bp in length
                                                                                                                                                         488 bp in length
                                                                                                                                                                                                           of 247 bp in length
                                                                                                                                                                                                                    unknown length
of 317 bp in length
                                                                                          a20 bp in len
11: contig of 1036 bp in len;
gap of unknown length
9: contig of 488 bp
gap of unknown length
cont.
                                                                                                                                                                                                                                                unknown length
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Best Local Similarity 100.0%; Pred. No. 9.6e-32;
Matches 79; Conservative 0; Mismatches 0;
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1. .24703
/organism="Homo sapiens"
/db_xref="taxon:9606"
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AF301505.1 GI:10086329
HTG; HTGS_PHASE1; HTGS_DRAFT.
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DEFINITION
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ORIGIN
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF301505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 24703)
105 Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
              AC010544 24703 bp DNA HTG 26-JAN-2000
Homo sapiens chromosome 16 clone RP11-447H7, LOW-PASS SEQUENCE
SAMPLING.
                                                                                                                                                                                                                                                                                                                                    NOTE: This record contains 38 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                         the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 637 bp in length
unknown length
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unknown length
of 497 bp in length
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of 345 bp in length
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unknown length
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of 312 bp in length
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unknown length
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unknown length
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unknown length
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of 211 bp in length
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AC010544.1 GI:5882394
HTG; HTGS_PHASE0.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 121067)
Taudien,S., Blaechschmidt,K., Menzel,U., Polley,A., Reichwald,K.,
Rump,A., Schilhabel,M.B., Schudy,A., Wen,G., Siebert,R.,
Schlegelberger,B. and Rosenthal,A.
Chromosome 8 genomic sequence
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                                                                                                                                                                                                             Submitted (31-A0G-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1232: gap of unknown length
2191: contig of 959 bp in length
2291: gap of unknown length
3307: contig of 1016 bp in length
3407: gap of unknown length
38915: contig of 35408 bp in length
64023: contig of 25108 bp in length
64023: gap of unknown length
64103: gap of unknown length
75307: contig of 11184 bp in length
75307: contig of 1184 bp in length
75407: gap of unknown length
91088: gap of unknown length
100156: contig of 1581 bp in length
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100156: gap of unknown length
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          +** SEQUENCING IN PROGRESS ***, 38
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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8348: gap of 100 bp

9400: contig of 1052 bp in length

9500: app of 100 bp

10588: contig of 1088 bp in length

10688: gap of 100 bp
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome, clone RP11-111L1
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92790: contig of 7655 bp in length
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92890: gap of
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103130: contig of 10240 bp in length
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103230: contig of 10240 bp in length
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109829
12599: gap of
100 bp
105829
125596: contig of 15868 bp in length
109829
125596: contig of 15868 bp in length
125697
125796: gap of
100 bp
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140801: contig of 15868 bp in length
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140801: contig of 15805 bp in length
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140801: contig of 15005 bp in length
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                                            17: gap of 100 bp
13151: contig of 1334 bp in length
51: gap of 100 bp
14779: contig of 1228 bp in length
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36876: contig of 2529 bp in length
36976: gap of 100 hn
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contig of 1733 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p of 100 bp contig of 1738 bp in length
11717: contig of 1029 bp in length
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/note="assembly_fragment"
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/note="assembly_fragment"
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85035: cont
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36977. 38709
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69925 . .75196
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21771. .24636
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10689. 11717
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vector_side:right"
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RESULT 20

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26-FEB-2001

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Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Cooke, P., DeArellano, M., Collymore, A., Cooke, P., DeArellano, W., Powarr, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatais, A., Klein, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Peterson, K., Pollaray, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Meeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Meeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Subramanian, B., Ye, W.J., Zimmer, A. and Zody, M., Sablon, L., Subritted (17-Nov-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 25, 2001 this sequence version replaced gi:12232534.

All repeats were identified using RepeatMasker:
Smit, A.F. A. & Green, P. (1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens chromosome 15 clone RP11-114F23 map 15, WORKING DRAFT SEQUENCE, 25 unordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160990)
                                                                                                                                                                                                                                                        0y 17555 caggetggtetegaaeteetgaeeteaggtgateeaeceeeeteageetecaaegtgtt 17614
                                                                                                                                                                                                                                                                                                                 DD 95877 CAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCACCCTCACCTCAGCCTCCCAAGTGTT 95936
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Center clone name: 114_F_23

Sequencing vector: M13; M77815; 10% of reads
Sequencing vector: M13; M77815; 10% of reads
Sequencing vector: Plasmid; n/a; 90% of reads
Chemistry: Dye-primer-amersham; 5% of reads
Chemistry: Dye-primer-amersham; 5% of reads
Chemistry: Dye-primer-amersham; 5% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 149544 bases at least Q40
Consensus quality: 157156 bases at least Q30
Consensus quality: 157159 bases at least Q20
Insert size: 166000; agarose-fp
Insert size: 166000; agarose-fp
Insert size: 166000; agarose-fp
Insert size: 176000; agarose-fp
Insert 
                                                   0.3%; Score 79; DB 65; Length 160210;
100.0%; Pred. No. 1.2e-31;
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Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
                                                                                                                                                     Indels
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                                                                             100.0%; Prea. ...
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                                                                                                       Best_Local Similarity 100.0
Matches 79; Conservative
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                                                        Query Match
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JOURNAL
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REFERENCE
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AC015664
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160210)
1 (bases 1 to 16021)
1 (
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Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.
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/clone_lib="RPCI human BAC library 11"
/note="This clone overlaps RP11-355D13 and RP11-315A19"
/ 36665 c 33372 g 42324 t 101 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 estimates computed by the phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
                                                        11-APR-2001
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Center code: UWMSC
Web Site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen6systemsbiology.org
Contact: Summary Statistics
Sequencing vector: pUCIB: L08752
Chemistry: Dye-terninator Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
Insert size: 155000; agarose-fp
Quality coverage: 10.9x in Q20 bases; sum-of-contigs
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                                                                                                  Homo sapiens chromosome 15 clone RP11-78121 map 15q15, ***
SEQUENCING IN PROGRESS ***, 2 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by the finished sequence as soon as it is available and the accession number will be preserved.

129675 contig of 129675 by in length 129676 129775; gap of unknown length 129776 160210; contig of 30435 bp in length.
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This entry has been annotated with sequence quality
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE2; HTGS_FULLTOP.
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                                         160210 bp
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JOURNAL
                                                                                                                                                                                                    ACCESSION
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KEYWORDS
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LOCUS
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                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                100 bp
of 1841 bp in length
of 1796 bp in length
100 bp
of 2112 bp in length
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88789 101600: contig of 12812 bp in length
101601 101700: gap of 100 bp
101701 115111: contig of 13411 bp in length
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6074: contig of 5669 bp in length

74: gap of 100 bp

74111: contig of 4937 bp in length
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83: gap of 100 bp
88688: contig of 7445 bp in length
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                                                                                                                                                                                                                                                                        181 280: gap of 100 bp
281 1445: contig of 1165 bp in length
1446 1545: gap of 100 bp
1246 3093: contig of 1548 bp in length
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14321: contig of 2566 bp in length
14421: gap of 100 bp
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63905: contig of 4633 bp in length
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1. .180
/note="assembly_fragment
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3094 3193; gap of
3194 5034; contig of 184
5135 5134; gap of 100 b
5135 6930; contig of 175
6931 7030; gap of 100
7031 9142; contig of 21
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/note="assembly_fragment"
3194. .5034
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/chromosome="15"
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1. .160990
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11655: cor
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homo sapiens chromosome 16 clone RP11-578P21, WORKING DRAFT
SEQUENCE, 17 unordered pieces.
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44409 a 34585 c 34521 g 45055 t
                                                       743. .11655
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88789. .101600
/note="assembly_fragment"
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9273. .63905
note="assembly_fragment"
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/note="assembly_fragment"
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.15212. .131102
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.43112. .158767
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.58868. .160990
                                                                                                                      4422. .17472
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Gaps

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COMMENT

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Direct Submission

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165173)
                                                                                                                                                                                                                                                                                                                    24628 CAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCACCCTCAGCCTCCCAAAGTGTT 24687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 37380 37379; contig of 37379 bp in length
* 37480 122440; contig of 84961 bp in length
* 122441 122540; gap of unknown length
* 122441 165173: contig of 42633 bp in length.
Location/Qualifiers
:ce 1. 165173
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Homo sapiens chromosome 16 clone RP11-167J20, WORKING DRAFT
SEQUENCE, 3 ordered pieces.
                                                                                                                                                                                            0.3%; Score 79; DB 68; Length 164353; 100.0%; Pred. No. 1.2e-31; ive 0; Mismatches 0; Indels 0;
/chromosome="16"
/clone="RP11-578P21"
/clone_iRP11-578P01 human BAC library 11"
48327 a 34627 c 33414 g 46311 t 1674 others
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.jgi.doe.gov
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HTG; HTGS_PHASE2; HTGS_DRAFT
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DOE Joint Genome Institute.
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                                                                                                                                                                                               Query Match 0.39
Best Local Similarity 100.0
Matches 79; Conservative
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                                                                                                                                   Tobes 1 to 164353)

DOE Joint Genome Institute.

Direct Submission

Submitted (BFEB-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA On Jul 13, 2000 this sequence version replaced 91:7211924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Consensus quality: 120365 bases at least 040
Consensus quality: 138510 bases at least 030
Consensus quality: 148253 bases at least 020
Estimated insert size: 149000; agarose-fp estimation
Estimated insert size: 162753; sum-of-contigs estimation
Quality coverage: 4.29 in 020 bases; agarose-fp estimation
Quality coverage: 3.93 in 020 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 17 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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gap of unknown length
contig of 25258 bp in length
gap of unknown length
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gap of unknown length
contig of 35316 bp in length.
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of 8463
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                                                                             Sequencing of Human Chromosome 16
Unpublished
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Center clone name: RPCI-11_578P21
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/db_xref="taxon:9606"
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Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
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RESULT 25
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On Apr 14, 2001 this sequence version replaced gi:13399355.

Center: Genome Center Center Center Center of Genome Center code: UWMSC Web site: UWMSC Web site: http://chroma.mbt.washington.edu/msg_www Contact: leerowen@systemsbiology.org

Contact: leerowen@systemsbiology.org

Contact: leerowen@systemsbiology.org

Contact: puc.Bib. L08752

Chemistry: Dye-terminator Big Dye; 90% of reads

Chemistry: Dye-terminator Big Dye; 10% of reads

Chemistry: Dye-terminator Big Dye; 10% of reads

Assembly program: Phrap: version 0.990399

Insert size: 180000; agarcse-fp

Quality coverage: 9.6x in Q20 bases; sum-of-contigs
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Rowen, L., Madan, A., Oin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Sequencing of human chromosome 15 D15S146-D15S117 region Unpublished
2 (bases 1 to 182608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B.,
Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G.,
James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.
                                                                                                                                                                                                                                                                                                                                                           Db 46174 CAGGCTGCTCGAACTCCTGACCTCAGGTGATCCACCCCACCTCAGCCTCCCAAGTGTT 46115
                                                                                                                                                                                                                                                                                                                            Qy 17555 caggetggtetegaaeteetgaeeteaggtgateeaeeeeaeeteageeteeaaagtgtt 17614
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0
                                                                                                                                                                                                                       Length 165173;
                                                                                                             208 others
                                                                                                                                                                                                                     0.3%; Score 79; DB 65; I
lilarity 100.0%; Pred. No. 1.2e-31;
Conservative 0; Mismatches 0;
/organism="Homo sapiens"
/db_xref="taxon:3606"
/chromosome="16"
/clone="RP11-167120"
i 35260 c 34381 g 45089 t
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HTG; HTGS_PHASE2; HTGS_FULLTOP
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Matches 79; Conserv
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* NOTE: This is a 'working draft' sequence. It currently * consists of 3 contigs. Gaps between the contigs

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Homo sapiens chromosome 12q clone RP11-1064P9, *** SEQUENCING IN
PROGRESS ***, 36 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy 17555 caggetggtetegaaeteetgaeeteaggtgateeaeceeaeeteageeteecaaagtgtt 17614
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved
* 1 25322 contig of 25322 bp in length
* 25323 27704: contig of 2282 bp in length
* 27705 27804; gap of unknown length
* 27705 27805 contig of 154804 bp in length.
                                                                                                                                                                                                                                                                                                                                   /clone="RPI1-355D13"
/clone_lib="RPCI human BAC library 11"
/note="This clone overlaps RPI1-402F9 and RPI1-78I21"
/ 33492 c 36932 g 51036 t 258 others
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                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
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Qy 17555 caggetggtetegaaeteetgaeeteaggtgatecaeceaecteageeteeeaaagtgtt 17614
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gap of unknown l
contig of 1114 b
gap of unknown l
contig of 1478 b
gap of unknown l
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gap of unknown l
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contig of 4360 b
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contig of 2866 b
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contig of 2866 b
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/db_xref="taxon:9606"
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/clone="RP11-1064P9"
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Matches 79; Conservative
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ORIGIN
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                 Martinez,E., Massey,E., Mayua,F., Martindar,F., Martindar,E.,
Martinez,E., Massey,E., Mayua,F., Martindar,E.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Near,Do., Newtson,J.,
Nowtson,N.,
Nguyen,A., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Oguh,M., Okwuon,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens, R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Soctt,G., Shen,H., Shooshtari,N.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Tang,H., Tansey,J., Taylor,C., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward'Moore,S., Warren,R., Washington,C.,
Wall,R., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: Estimated insert size may differ from sequence length

* (see http://www.ngsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "vorking draft' sequence. It currently

* consists of 36 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Connections and the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jan 5, 2001 this sequence version replaced gi:11415095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig of 15177 bp in length gap of unknown length contig of 13130 bp in length contig of 1304 bp in length gap of unknown length gap of unknown length
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f unknown length
of 10096 bp in length
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g of 7633 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Baylor College of Medicine
Center code: BCM
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of 6624 b
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gap of unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Worley, K.C.
Direct Submission
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0; Gaps

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS MEDLINE COMMENT

JOURNAL

TITLE

RESULT 26

G42927/c

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Direct Submission

Direct Submission

Calo 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requestes: clonnereques/@sanger.ac.uk

On Oct 27, 1999 this sequence version replaced gi:601555.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbrevlations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information
on the WORMMEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence is
the entire insert of clone RPS-8426 This sequence was generated
from part of bacterial clone contigs of human chromosome 20,
constructed by the Sanger Centre Chromosome 20 Mapping Group.
Further information can be found at
http://www.sanger.ac.uk/HGPC/Chr20
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by yat least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. RP5-84266 is from the
further details see
http://www.chori.org/bacpac/home.htm
VECTOR: PCTOR: 
                                                                                                                                                                                                                                                                                                                                                                                                HSDJ842G6 100272 bp DNA PRI 04-APR-2001
Human DNA sequence from clone RP5-842G6 on chromosome 20. Contains the 3' end of a novel gene, the 3' end of the gene for a novel protein similar to SELLE (sel-1 (suppressor of lin-12, C.elegans)-like), ESTs, STSs and GSSs, complete sequence.
AL109657.8 GI:6136991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100272)
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/note="MER63A repeat: matches 109. .210 of consensus"
join(<1831. .1878,3489. .3592,7112. .7151,10137. .10334,
17493. .17553,25114. .25197,25526. .25608,25769. .27072)
                                                                                           26373 accagagacaagcagagtaacaggatcagtgggtctaagtgtccgagacttaacgaaaat 26432
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/note="MER63A repeat: matches 57. .201 of consensus"
835. .922
                                                                                                                                                  78 ACCAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCGAGACTTAACGAAAAT 19
                                      Indels
100.0%; Pred. No. 1.....+ive 0; Mismatches 0;
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/db_xref="taxon:9606"
/chromosome="20"
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                                                                                                                                                                                                    Best Local Similarity 100.0
Matches 78; Conservative
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HSDJ842G6/c
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                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 137)
1 (bases 1, Fan,J.B., Siao,C.J., Berno,A., Young,P., Sapolsky,R., Ghandour,G., Perkins, W., Winchester,E., Spencer,J., Kruglyak,L., Stein,L., Hsie,L., Topaloglou,T., Hubbell,E., Robinson,B., Mitmann,M., Morris,M.S., Shen,N., Kilburn,D., Rioux,J., Nusbaum,C., Rozen,S., Hudson,T.J., Lipshutz,R., Chee,M. and Lander,E.S.
                                                                                                                                                                             G42927 137 bp mRNA STS 27-JAN-1999
WIAF-176-STS Human THudson EST Homo sapiens STS cDNA, sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/map="36.40 cR from top of Chr17 linkage group"
/clone_lib="Human THudson EST"
/note="STSs derived from sequences in dbEST and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 degrees C for 4.00 minutes 94 degrees C for 50.0 seconds 58 degrees C for 1.50 minutes 72 degrees C for 1.00 minutes 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Large-scale identification, mapping, and genotyping of single-nucleotide polymorphisms in the human genome Science 280 (5366), 1077-1082 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synonyms: EST226740b, EST226740
Contact: Thomas Hudson
Whitehead Institute/MTT Center for Genome Research
Whitehead Institute for Biomedical Research
Whitehead Institute for Biomedical Research
Tel: 617, 252, 1900
Fax: 617, 252, 1902
Email: thudson@genome.wi.mit.edu
Primer A: TATTGCAGCTGAAATATTTTCG
Primer B: AAGTCATGGAAACAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 137;
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each 5
4 nM
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Polymerization:
     Db 42715 GGGATTACAGGCGTGAGCC 42697
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Gelatin:
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PCR Profile:
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primer_bind
BASE COUNT 2
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Query Match

source

FEATURES

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/note="MLT1H repeat: matches 39. .538 of consensus"
join(<10194. .10334,10469. .10524,17493. .17553,23069. .23166,
25114. .25197,25526. .25608,25769. .25879)
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/evidence=not_experimental
/product="dJ84266.13"
/product="dJ84266.13"
/gene="dJ84266.13"
/gene="dJ84266.13"
/gene="dJ84266.13"
/gene="dJ84266.13"
/gene="dJ84266.13"
/gene="dJ84266.13"
/gene="dJ84266.13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anote="Charlield repeat: matches 114. .318 of consensus"
12430. .12737. .13028

Anote="Charlield repeat: matches 1. .301 of consensus"
13187. .13028

Anote="Charlield repeat: matches 1. .314 of consensus"
13187. .13362

Anote="Limbl repeat: matches 5675. .5851 of consensus"
13187. .13460

Anote="Limbl repeat: matches 2650. .2750 of consensus"
14830. .14586

Anote="Aluy repeat: matches 1. .291 of consensus"
14877. .15185

Anote="Aluy repeat: matches 1. .300 of consensus"
15560. .15996

Anote="Aluy repeat: matches 1. .298 of consensus"
15699. .15996

Anote="Aluy repeat: matches 1. .298 of consensus"
16134. .1613

Anote="Aluy repeat: matches 1. .294 of consensus"
16134. .1613

Anote="Match: STS: Em:N51549"

Anote="Match: STS: Em:N51549"

Anote="Li repeat: matches 2559. .2735 of consensus"
17634. .17807

Anote="Li repeat: matches 2559. .2735 of consensus"
17634. .17807

Anote="Li repeat: matches 4. .2505 of consensus"
17842. .21371
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/note="Charlielb repeat: matches 314. .518 of consensus"
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21599. .21890
/note="Alusx repeat: matches 11. .302 of consensus"
22131. .22545
/note="L2 repeat: matches 2267. .2730 of consensus"
22734. .22855
/note="MR repeat: matches 9. .131 of consensus"
join(<22068. .25197, 25526. .25608, 25769. .2879)
/gene="dJ84266.1"
                                                                                                                                                                                                                                      /note="match: ESTs: Em:AA610002"
/evidence=not_experimental
/product="d1842G6.1.4 (novel protein (isoform 4))"
11038 .11341
/note="AluSq repeat: matches 1. .302 of consensus"
12044 .12049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: ESTs: Em:AA846518"
/widence=not_experimental
/product=nd484266.1.5 (novel protein (isoform 5))"
25857. .25862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 83. .174 of consensus"
21395. .22112
/gene="dJ842G6.1"
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                                                                                                                                                                                                                                                                                                                                                             /gene="dJ842G6.1"
12219. .12429
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27053. .27058
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/gene="dJ842G6.1"
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                                mRNA
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match: ESTs: Em: BB093902 Em: BE756623 Em: AV999810
Em: AK062306 Em: AL0634906 Em: AL335272 Em: AN9806074 Em: N32022
Em: BF514413 Em: AL1646144 Em: W44769 Em: AL026801 Em: BF51400 Em: BE569917 Em: AL000893 Em: AL036801 Em: BF415063
Em: BE554400 Em: BE669917 Em: AL000893 Em: AL036721
Em: BE554400 Em: BE208434 Em: AL326823 Em: AL026396
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join(<1831. 1878, 3489. 3592, 7112. 7751, 10137. 10334, 11493. 17553, 23069. 23094, 25114. 25197, 25526. 25608,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="ETIGKFFQADIAENALKNSSETEIPTVSVLADEEFLPFKENTFD
LVSSLSLAHWVNDLPRALEQQHYILKPOGVFCADMEGGPTLFELRGSLQLAETRERGG
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RKALLHRDTMLAAAAVYREMYRNEDGSVPATYQIYYMCGWYHESQARPAERGSATVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="ETIGKFPQADIAENALKNSSETEIPTVSVLADEEFLPFKENTFD
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Em:A1659843 Em:A1379944 Em:AI092608 Em:AA789132"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(<1831. .1878,3489. .3592,7112. .7151,10137. .10334,
17493. .17553,2514. .25197,25526. .25608,25769. .25861)
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17493. .17553,23069. .23094)
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/note="WER81 repeat: matches 41. .114 of consensus"
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Anote-"L2 repeat: matches 1663. .1749 of consensus"

complement(8958. .9098)

/note-"match: GSS: Em:AQ631427"

9324. .9793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2928. .3229
Anote-"Alux repeat: matches 1. .305 of consensus" complement(312. .3526)
Anote-"match: GSS: Em:AQ631367"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3662. .3818
/note="AluSx repeat: matches 1. .155 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .286 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="dJ842G6.1"
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2928. .3229
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/note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGELGKINNLMPPGKKSQ"
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TITLE
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KEYWORDS
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Center: Whitcher Gone, Wilker, M. Tenter for Genome Research Santi, A. R. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 141708)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone RP11-262B3
ACU24993 141708 bp DNA HTG 10-JAN-2001
HOMO sapiens Chromosome 8 clone RP11-262B3 map 8, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M33, M77815; 69% of reads Sequencing vector: Plasmid; n/a; 31% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 14185 bases at least Q40 Consensus quality: 14162 bases at least Q30 Consensus quality: 14167 bases at least Q30 Insert size: 135000; agarose-fp Insert size: 14608; sum-of-contigs Quality coverage: 13.1 in Q20 bases; agarose-fp
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Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE, 2 ordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC024993.4 GI:12061519
                                                                                                                                                                   11252 GCCTCCCGGGTTCAAGCA 11235
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                                                                                                                               Qy 17434 gcctcccgggttcaagca 17451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
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JOURNAL
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KEYWORDS
SOURCE
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COMMENT

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AC015520 180052 bp DNA HTG 09-SEP-2000
Homo sapiens clone RP11-23C19, WORKING DRAFT SEQUENCE, 41 unordered
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Boukhgalter, B., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Costle, A., Castle, A., Callins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreiar, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Howland, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Llehockky, J., Lleu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGwan, P., McGwan, Y., Norman, C.H., O'Connor, T., O'Donnell, P.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180052)
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Quality coverage: 12.5 in Q20.

* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is balieved to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 2033 2132: gap of 100 bp

* 2033 2132: gap of 100 bp

* 11708: contig of 139576 bp in length.
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Unpublished
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1. .2032
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Best Local Similarity 100.0%; Pred. No. 4.4e-31
Matches 78; Conservative 0; Mismatches 0
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38281 a 28210 c 29655 g 45462 t
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AC015520
AC015520.3 GI:10045465
HTG; HTGS_PHASE1; HTGS_DRAFT.
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1. .141708
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TITLE JOURNAL COMMENT

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156954 173334 contig of 18181 bp in length
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140779 154853: contig of 14075 bp in length
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130749: contig of 14892 bp in length
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f 6307 bp in length
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180052: contig of 6818 bp in length.
                                                                                             89: gap of 100 bp
29265: contig of 1376 bp in length
                                                                                                                                                                                                                                                                        83: gap of 100 bp 40142: contig of 2759 bp in length
                                                                                                                                                                                                                                                                                                          42: gap of 100 bp 43686: contig of 3444 bp in length
                                                                                                                                                                                                                                                                                                                                           ap of 100 bp contig of 3302 bp in length
                                                                                                                                                                                                                                                                                                                                                                            88: gap of 100 bp 52035: contig of 4847 bp in length
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102195: contig of 8738 bp in length
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130850 140678: contig of 9829 bp in length
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                         14: gap of 100 bp
26113: contig of 2199 bp
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32181: contig of 2816 bp
                                                                                                                                                                   p of 100 bp
contig of 1420 bp
                                                                                                                                                                                                    ap of 100 bp
contig of 1478 bp
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37283: contig of 1904 bp
                                                          13: gap of 100 bp
27789: contig of 1576 bp
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55272: cont
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                                                                                      Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 9, 2000 this sequence version replaced gi:6642701.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                      Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR Neb Site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 3.9 in Q20 bases; agarose-fp Quality coverage: 3.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                     Center clone name: 2_c_19

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 15371 bases at least Q40
Consensus quality: 1765735 bases at least Q30
Consensus quality: 170554 bases at least Q20
                                                                                                                                                                                                                                                                      p of 100 bp in length contig of 100 bp in length contig of 1067 bp in length p of 106 bp p of 109 bp in length contig of 109 bp in length p of 109 bp of 100 bp
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contig of 1008 bp in length
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Insert size: 176052; sum-of-contigs
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20340:
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17795:
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14157: con
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21690: con
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3786: con
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Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
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63507
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                    TITLE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 213943)
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100.0%; Pred. No. 4.6e-31;
ive 0; Mismatches 0;
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13127. .14157
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Matches 78; Conserva
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AC015465
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AUTHORS
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JOURNAL
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AUTHORS
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SOURCE
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δλ

δ QQ

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Direct Submission
Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 10, 2000 this sequence version replaced g1:7341762.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 177000; agarose-fp
Insert size: 210943; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                  Web size that the property of the property of the project of the project name: 2255

Center clone name: 12255

Center clone name: 35_A_5

Center clone name: 15_A_5

Consensus quality: 2032727 bases at least Q40

Consensus quality: 2032727 bases at least Q30

Consensus quality: 203273 bases at least Q30
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23550 27145: contig of 3596 bp in length
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contig of 3785 bp in length
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31131 34297: contig of 3167 bp in length
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contig of 3323 bp in length
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53118 57744: contig of 4627 bp in length
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19843 23449: cont
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53017: con+
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38391 41958: conf
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57745 57844: gap of
57845 63406: cont
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209156 209255: gap of 100 bp
209256 213943: contig of 4688 bp in length.
Location/Qualifiers
                                                                                 104655 104754: gap of 100 bp
104755 110937: contig of 6183 bp in length
110938 111037: gap of 100 bp
111038 117971: contig of 6934 bp in length
                                               292: gap of 100 bp
104654: contig of 8362 bp in length
                            bp in length
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96192: contig of 6095
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Brown, J.

Direct Submission

Submitted (30-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBLO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
Submitted (30-JAN-2001) Sanger car.uk
CBLO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
on Oct 1, 2000 this sequence version replaced gi:8247074.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: FMBL; Sw: SMISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
has been finished according to sequence map criteria as follows.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL136969 79666 bp DNA PRI 11-APR-2001 Human DNA sequence from clone RP1-207J11 on chromosome 7 Contains ESTs and STSs. Contains two zinc finger protein pseudogenes, a putative novel gene and an HNRPC (heterogeneous nuclear ribonucleoprotein C (C1/C2)) pseudogene, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 79666)
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100.0%; Pred. No. 4.7e-31;
ive 0; Mismatches 0; Indels 0;
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TITLE
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KEYWORDS
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Sw:Q05481 Tr:Q02313

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An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annoctated repeat sequence elements. Where the sequence is annotation using the 'unsure' feature key. RP1-207J11 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm vECTOR: pcYPAC2
IMPORTANT: This sequence is the entire insert of clone RP1-207J11 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP1-207J11 is at 1 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / 0063. .5395 / Orde="Link8 repeat: matches 4441. .5788 of consensus" 5621. .5904 / Orde="Link8 repeat: matches 12. .309 of consensus" 5621. .5905. .6560 / Orde="BURI repeat: matches 10970. .11628 of consensus" 6612. .6866 / Orde="BURI repeat: matches 10970. .11628 of consensus" 6614. .6869 / Orde="BURI repeat: matches 10733. .10985 of consensus" / Orde="MER93 repeat: matches 268. .371 of consensus" / Orde="Alug repeat: matches 1. .296 of consensus" / Orde="Alug repeat: matches 1. .268 of consensus" / Orde="MER93 repeat: matches 1. .268 of consensus" / Orde="BURI repeat: matches 1. .268 of consensus" / Orde="BURI repeat: matches 9897. .10662 of consensus" / Orde="BURI repeat: matches 9897. .10
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/note="AluSg repeat: matches 1. 305 of consensus"
3462. 33936
/note="LiMa8 repeat: matches 5816. 6287 of consensus"
4063. 5395
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"note="BUR1 repeat: matches 9606. .9912 of consensus"
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7.00te="LTR15 repeat: matches 357. .493 of consensus" 2451. .2618
7.00te="LTR4 repeat: matches 245. .406 of consensus" 2489. .2659
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/note="AluSx repeat: matches 1. .293 of consensus"
join(11584. .13098,13420. .13705,13831. .13917)
/gene="dJ207J11.1"
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match: cDNAs: Em:AB040906
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/gene="dJ207J11.1"
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note="match: STS: Em:G06001"
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/chromosome="7"
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/clone_lib="RPCI-1"
320. .692
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27104. .27159
/note="HUERS-P3b repeat: matches 3446. .3510 of consensus"
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16573. .16885
/note="AluSq repeat: matches 1. .312 of consensus"
17633. .17936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6250. .6306 of consensus"
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18579. .18610
//octe="16 copies 2 mer at 93% conserved"
18611. .18921
//octe="Alux repeat: matches 1. .311 of consensus"
18932. .18980
//octe="Alux repeat: matches 6238. .6286 of consensus"
18981. .19287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Alusc repeat: matches 1. .307 of consensus"
19288. .22366
/note="LiP5 repeat: matches 3193. .6238 of consensus"
22367. .22699
/note="Alux repeat: matches 1. .311 of consensus"
22700. .22856
                                                                                                                                                                                                                                                 /evidence=not_experimental
13103. .13403
/note="Alux repeat: matches 1. .301 of consensus"
14125. .14397
/note="Alusp repeat: matches 1. .307 of consensus"
14781. .15076
/note="Alusx repeat: matches 1. .296 of consensus"
15418. .15474
/note="Libday repeat: matches 6250. .6306 of consensus"
15493. .15764
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24137. .24687
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/note="AluSp repeat: matches 1. .303 of consensus"
/note-"AluSp repeat: matches 1080. .1228 of
/note="MER57-internal repeat: matches 1080. .1228 of
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/note="AluSq repeat: matches 1. .311 of consensus"
27736. .28880
/note="MER51-internal repeat: matches 3767. .4921 of
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/note="MER51-internal repeat: matches 3587. .3767 of
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/note="MER57-internal repeat: matches 2476. .2626 of
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24690. .25772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Alusx repeat: matches 4. .273 of consensus"
15774. .15921
match: proteins: Tr:Q9Y2Q1 Tr:Q9UII5 Sw:Q05481 Tr:
Sw:Q03923 Tr:Q43345 Tr:Q9Y2NB Tr:Q052523 Sw:P51522
Sw:Q99676 Sw:P28160 Tr:Q050792 Tr:Q9Y6R6 Sw:Q15928
Tr:Q65212 Tr:C43693 Tr:C9UBL4 Sw:Q75820 Tr:Q4186
Tr:Q55779 Sw:Q1462B Tr:Q9YBL4 Sw:Q75820 Tr:Q1486
Tr:Q05374 Sw:P08045 Sw:P16415 Tr:Q61491 Tr:Q9ULS9
Sw:Q03924 Sw:P08053 Tr:C9C479 Tr:Q0UL37 Tr:Q9G14
Tr:Q06054 Tr:Q14593 Tr:P97672 Tr:Q6510 Sw:P17097"
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Anote-"Alusg repeat: matches 3. .302 of consensus"
26511. .26961
Anote-"MER57-internal repeat: matches 1228. .2371
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/note="MER57-internal repeat: matches 3336.
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28238. .30656
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AC073283 175197 bp DNA HTG 07-AUG-2000
Homo sapiens chromosome 2 clone RP11-761B3, WORKING DRAFT SEQUENCE,
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Eukaryotą; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Consensus quality: 143624 bases at least Q40
Consensus quality: 145128 bases at least Q30
Consensus quality: 146083 bases at least Q20
Insert size: 147000; agarose-fp
Insert size: 143396; sum-of-contigs
Quality coverage: 4.60 in Q20 bases; agarose-fp
Quality coverage: 4.61 in Q20 bases; sum-of-contigs
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/db_xref="taxon:9606"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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  /note="MER41-internal repeat: matches 1449. .3944 of
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/note="AluSg repeat: matches 3. .138 of consensus"
33831 .34136
/note="AluSg repeat: matches 1. .303 of consensus"
34321 .34433
34322 .34433
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Submitted (16-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
Mo 63108, USA
On May 11, 2000 this sequence version replaced gi:7715653.
                                                30673. .31219
/note="MER41A repeat: matches 1. .554 of consensus"
complement(join(31775. .32111,32424. .32482))
/note="match: STS: Em:G61808"
32095. .32387
                                                                                                                                                                                /note="AluSx repeat: matches 5. .297 of consensus" 33085. .33128
/note="MBR4-internal repeat: matches 751. .794 of
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/note="MER4-internal repeat: matches 354. .465
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/note="MER4-internal repeat: matches 465.
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100.0%; Pred. No. 1.7e-30;
itive 0; Mismatches 0; Indels 0;
39298 103965: contig of 14668 bp in length 33966 104065: gap of unknown length 4066 115054: contig of 10989 bp in length 51055 115154: gap of unknown length 5155 128256: contig of 13102 bp in length 8157 128356: gap of unknown length 8157 142378: contig of 14022 bp in length 2379 142478: gap of unknown length 279 175197: contig of 32719 bp in length 17197: contig of 32719 bp in length. 1.175197
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17529. 21904
7note="assembly_name:Contig45"
22005. 27180
7note="assembly_name:Contig46"
27281. 30585
7note="assembly_name:Contig47"
30686. 36202
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/note-assembly_name:Contig52"
72024 . 81310 /note-"assembly_name:Contig53"
81411 . 89197 /note-"assembly_name:Contig54"
89298 .103965
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115155..128256
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128357..142378
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142479..175197
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/note="assembly_name:Contig40"
4174. 7642
/note="assembly_name:Contig41"
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104066. .115054
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/note="assembly_name:Contig42"
10912. 13683
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40217 c 38462 g 47738 t
                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-761B3"
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Matches 77; Conservative
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                                                                                                               Direct Submission
Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MM 63108, USA.
On Aug 7, 2000 this sequence version replaced gi:9653223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                 Sequencing vector: M13: 100%
Sequencing vector: plasmid; 0%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer E7: 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 166975 bases at least Q40
Consensus quality: 170804 bases at least Q20
Insert size: 156000; agarose-fp
Insert size: 173197; sum-of-contigs
Quality coverage: 5.57 in Q20 bases; sum-of-contigs
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Waterston, R.H.
                                                                                   2 (bases 1 to 175197)
Waterston, R.H.
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Gaps

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I (Dassas I to 17622)

MULLY, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Adio-Oduola, B., Ali-Osman, F.R., Barbaria, J., Barton, J., Bimage, K., Blanken, T., Barderia, J., Barton, J., Burach, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, J., Burch, B. Burch, J., Burch, J., Burch, J., Charde, C., Carron, F.F., Carter, M., Cavazoos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, G., Chen, G., Chen, G., Chen, C., Carter, M., Cavazoos, S.R., Chacko, J., Chavez, D., Chan, G., Chen, G., Chen, G., Chen, C., Coyle, M.D., Dathorne, S.R., David, R.V., Depar, H.J., Dugan, Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Elhaj, C., Emerling, S., Escotto, M., Farlis, T., Ferraquoto, D., Flagg, N., Ford, J., Forster, P., Ferraquoto, D., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, M., Garrath, P., Hande, S., Hamilton, K., Han, J., Harris, K., Hartt, M., Haylak, P., Hares, A., Hernandez, J., Hernandez, G., Hader, J., Howard, S., Huber, J., Hollyk, S., Hume, J., Ioshikhes, I., Jacobson, B., Jia, Y., Johnson, R., Marlindale, A., Martindale, A., Martindale, A., Martindale, A., Martindale, A., Martindale, R., Martindale, A., Martindale, R., Martindale, A., Martindale, A., Martindale
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                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176626)
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INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                    ACO84754 176626 bp DNA PRI 01-JAN-2001
Homo sapiens 12p BAC RPI1-874G11 (Roswell Park Cancer Institute
                                                                                                        Human BAC Library) complete sequence. AC084754
                                                                                                                                                                                                              AC084754.14 GI:12000447
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RESULT 34
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (GNC. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Feprits of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

QUALSTAT-REPORT------

atatatatac(a)ctattataca tactcacagg(t)acagacacta taccaatgaa(t)gattttattc cctaaaatgc(t)gagtataata tttcttcttc(t)tttttttttt cattctattg(t)cgtctttcta gatacctttg(t)ctataattca ttaagataaa(g)ggattatcct ctaagggaag(a)ctttgttaag aatgattíta(t)ícattttaaa ttttactgtg(t)tgagatatgt atgttcatca(g)ggttattggt gttccgcttt(c)ttcgtgcacc cgtctttcta(a)aactgaggaa ccaatcttaa(g)aggggtggaa aatcttaaga(g)gggtggaagg tcttaagagg(g)gtggaaggaa cttaagaggg(g)tggaaggaaa ttaagaggg(t)ggaaggaaac tgttttatta(g)gcatgacctt cacttatagg(t)gggaattgaa tgttgtgggg(t)gggggggggg 999199999(a)999999999 gttgtggggt(g)gggggagggg 176626 175830 1.84818e-05 0.0105784 Edited+Context Summary Statistics ------Consensus changing edits Phrap values in estimate:
Average error rate (BCM-Phrap estimate):
Fraction of Phrap values less than 40:
Number of consensus changing edits: tttfactgtg(n)tgagatatgt atgtccaca(n)ggttattggt gttccgcttt(n)ttcgtgcacc cctaaaatgc(n)gagtataata ttctctctc(c)ttttttttt cattctattg(n)cgtcttcta cgtctttcta(n)aactgaggaa ttaagataaa(n)ggattatcct atatatatac(n)ctattataca tactcacagg(n)acagacacta aatcttaana(n)gnnnggaagg tcttaanang(n)nnggaaggaa gatacctttg(n)ctataattca ctaagggaag(n)ctttgttaag taccaatgaa(n)gattttantc aangatttta(n)tcattttaaa ccaatcttaa(n)angnnnggaa cttaanangn(n)nggaaggaaa ttaanangnn(n)ggaaggaaac tgttttatta(n)gcatgacctt aggaggggg (n) agggggnnggg cacttatagg(n)gggaattgaa tgttgtgggg(n)ngggggnngg gttgtggggn(n)gggggnnggg Original+Context Number of consensus changin Number of N's in consensus Contig length: Position 145142 153486 153497 155105 155107 155109 172601 172670 172671 172677 165603 25566 55111 3638 60346 73890 74086 74094 31729 51964

ggtggggga(g)gggggaggga

ggnngggggn(n)gggggaggga

Department

gc-help@bcm.tmc.edu

COMMENT

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                         Distribution of Quality < 40 Bases
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Phrap Value Range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.3%; Score 77; DB 88; 100.0%; Pred. No. 1.7e-30; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                        1. .176626
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778. .1192

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complement(3679. .3715)

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complement(3716. .4018)

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4068...4101
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complement(4102...4198)
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6022. .6692
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RESULT 35 AC022202/c

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Direct Submission
Submitted (26-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 222548)
Waterston,R.H.
AC022202 222548 bp DNA HTG 22-MAR-2001
Homo sapiens chromosome UNK clone RP11-321E8, WORKING DRAFT
SEQUENCE, 2 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 2 conflags. The true order of the pieces and thouse and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                MO 63108, USA
On Mar 22, 2001 this sequence version replaced g1:12830304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.3%; Score 77; DB 67; Length 222548; 100.0%; Pred. No. 1.7e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center
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1. 222548: contig of 133480 bp in length. 1. 222548

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//db.xref="taxon:9606"
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/note="assembly_name:Contig18
clone_end:T7
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/note="assembly_name:Contig19
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89069. .222548
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Best Local Similarity
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.-418 of consensus"

.385 of consensus"

.762 of consensus"

.3130 of consensus"

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/note="LlPBa repeat: matches -1540. .-1343 of consensus"
2610. .3148
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/note="Alusg/x repeat: matches 150. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anote-"Alusg/x repeat: matches 135. .302 of consensus." 12814. .13041
Anote-"L2 repeat: matches 1920. .2147 of consensus." 13059. .13482
                                                                                                                                                                                                                                                        6413. 7207

/note="L1 repeat: matches 3127. 3925 of consensus"

7196. 7759

/note="L1M repeat: matches 4763. 5327 of consensus"

7770. 8144
                                                                                                                                                                                   3142. .4190
/note="LiPBa repeat: matches -279. .762 of consensus
4191. .4504
470te="LiUYD8 repeat: matches 1. .313 of consensus"
4505. .4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /770. 8144
/note="MSTB repeat: matches 1. .386 of consensus"
8146. 8425
/note="Alusg repeat: matches 1. .280 of consensus"
8442. 8495
/note="MSTB repeat: matches 373. .426 of consensus"
8496. .10087
/note="MSTB-internal repeat: matches 1. .1651 of con
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13997. .14416
1700te="MYTB repeat: matches 1. .426 of consensus"
14440. .14485
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13551. .13728
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'note="Alusg repeat: matches 5. .303 of consensus"
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/note="MSTB repeat: matches 1. .426 of consensus"
11054. .11346
/note="Alusx repeat: matches 1. .293 of consensus"
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/note="119 copies 2 mer aa 71% conserved"
/17956. .18395
/note="match: STS: Em:G50245"
19042. .19527
                                                                    copies 2 mer ga 81% conserved"
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                                                                                                                                         1610. .3148
/note="L1PBa repeat: matches -940.
                                                                                                                                                                                                                                                                                                                                                                                             1189.
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/note="11PBa repeat: matches 6252. .6412
                                                                  /note="68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (07-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, Caudmisted (07-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerquest@sanger.ac.uk
On Apr 8, 2001 this sequence version replaced gi:13366339.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either duble stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSRROT; Tr:, TREMBL; WP: WORMPEP; Information on the WORMPEP database can be found at
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/RGP/Chr9
RP11-507D14 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
http://www.chori.org/bacpac/home.htm
VECTOR: pBAGe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-507D14 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP11-507D14 is at 1 in this sequence. The true left end of clone RP11-299M1 is at 11585 in this sequence. The true right end of clone RP11-299M1 is at 131585 in this this sequence.
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Primates; Catarrhini; Hominidae; Homo.
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                                                                                         29173 TGAGACGGAGTTTCACTCTTGTTGCCCAGGCTGGAGTGCAATGGCGTGATCTCAGCTCAC 29114
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e-anence from clone RP11-507D14 on chromosome
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/db_xref="taxon:9606"
/chromosome="9"
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9q21.2-22.1, complete sequence.
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Mammalia; Eutheria; Primates;
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/clone="RP11-507D14"
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Direct Submission
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.1651 of consensus"

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32706. .32965
/note="LiMc5 repeat: matches 6960. .7215 of consensus"
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2966. 30150
/note="Alusp repeat: matches 1. .296 of consensus"
30151. 301387
/note="LIM4 repeat: matches 2274. .2506 of consensus"
30168. 30689
/note="Aluso repeat: matches 1. .295 of consensus"
30690. 30727
/note="LIM4 repeat: matches 2506. .2223 of consensus"
30690. 30727
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/note="AluSg repeat: matches 1. 309 of consensus"
31037. 31237. 31238
/note="LiM4 repeat: matches 2222. 2414 of consensus"
31264. 31459
/note="LiM4 repeat: matches 2466. 2669 of consensus"
31460. 31759
/note="AluSg repeat: matches 3. 307 of consensus"
31760. 31926
/note="LiM4 repeat: matches 3. 307 of consensus"
31760. 31926
/note="LiM4 repeat: matches 2669. 2833 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L1M1 repeat: matches 1515. .1586 of consensus"
28220. .28530
/note="MER39b repeat: matches 89. .579 of consensus"
19528. .19836
105te="Aluga repeat: matches 1. .300 of consensus"
19837. .19924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Alusx repeat: matches 1. .312 of consensus". 29414. .29703
/note="Alusg repeat: matches 1. .290 of consensus" 29705. .29746
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/note="MLT1F repeat: matches 10. .539 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                  .306 of consensus"
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27321. .27633
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32354. .32679
                                                                                                                                                                                                                                                                                                                                                                            /note="AluSg repeat: matches 1.
26032. 26316
/note="AluSx repeat: matches 1.
26891. 26941
/note="17 copies 3 mer act 72% cc
26963. 27123
                                                                                                                                                                                                                                                                                                                                         /note="L2 repeat: matches 2451.
25584, .25891
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'note="L1ME3 r
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Query Match

0.3%; Score 76; DB 89; Length 131684;
Best Local Similarity 100.0%; Pred. No. 5.8e-30;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 17555 caggetggtetcgaactectgacctcaggtgatccaccacctcagacttccaaagtgtt 17614
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1. .134601

source

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 134601) Plumb, B. Submitted (25-FFB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 28, 2001 this sequence version replaced gi:13161694. 26-FEB-2001 Assembly program: XGR44; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Sequencing vector: plasmid; L08752; 100% of reads Consensus quality: 13362 bases at least Q40 Consensus quality: 133079 bases at least Q30 Consensus quality: 133350 bases at least Q30 Insert size: 133801; sum-of-contigs Insert size: 13723; 2.3% error; agarose-fp Quality coverage: 6.99x in Q20 bases; sum-of-contigs Quality coverage: 6.90x in Q20 bases; sum-of-contigs Quality * NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the apps are unknown. * This record will be updated with the finished sequence * soon as it is available and the accession number will 24781 24880: gap of 100 bp 24881 33578: contig of 8698 bp in length 33679 3674: gap of 100 bp 25575 62674: gap of 100 bp 104203 104302: gap of 100 bp 104303 109696: contig of 5394 bp in length 109697 109796: gap of 100 bp 109797 115697: contig of 5901 bp in length 115798 134601: contig of 18804 bp in length. Location/Qualiflers 24780: contig of 24780 bp in length 93786 93885: gap of 100 bp 93886 104202: contig of 10317 bp in length AL450106 134601 bp DNA HTG Homo sapiens chromosome 9 clone RP11-280P22, PROGRESS ***, 9 unordered pieces. Web site: http://www.sanger.ac.uk Contact: humquery@sanger.ac.uk ------ Project Information Center project name: bA280P22 AL450106.8 GI:13162034 HTG; HTGS_PHASE1; HTGS_DRAFT Center code: SC as soon as ic Homo sapiens human. LOCUS DEFINITION AUTHORS TITLE ORGANISM 17615 ACCESSION REFERENCE JOURNAL VERSION KEYWORDS SOURCE AL450106 FEATURES COMMENT δy

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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 127417 CAGGCTGGTCTCGAACTCCTGACCTCAGGTGCACCCACCTCAGCCTCAAAGTGTT 127476
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 149386)
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Homo sapiens chromosome 4 clone RP11-211G17 map 4, WORKING DRAFT
SEQUENCE, 19 unordered pieces.
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0
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5.8e-30;
hes 0;
                                                                                                                                                                                                                                                                             4.00 to the first section of the fragment. 13.15 for the fragment. Chain: 1" 13.67 for the fragment. Chain: 1" 10.0218 fragment. Chain: 2" 10.0251 fragment. Chain: 2" 10.0351 fragment. Chain: 2" 10.
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fragment_chain:2"
10997. _115697
/note="assembly_fragment:00556
fragment_chain:2"
_115798. _134601
/note="assembly_fragment:00926
fragment_chain:2
                                                                                                                           1. .24780
/note="assembly_fragment:01918
fragment_chain:1
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a 28400 c 29106 g 36859 t
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100.0%; Pred. No. 5.8
ive 0; Mismatches
                                                                                         /clone_lib="RPCI-11.1"
/db_xref="taxon:9606"
                          /chromosome="9"
/clone="RP11-280P22"
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AC040997.2 GI:7770615
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Best Local Similarity 100.0
Matches 76; Conservative
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ORIGIN
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AUTHORS
TITLE
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AUTHORS
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KEYWORDS
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: 19525
Center clone name: 211_G_17
Center clone name: 211_G_17
Center clone name: 211_G_17
Sequencing vector: M13: M7815; 100% of reads
Sequencing vector: M13: M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 143909 bases at least Q40
Consensus quality: 145966 bases at least Q20
Insert size: 151000; agarose-fp
Insert size: 151000; agarose-fp
Insert size: 151000; agarose-fp
Quality coverage: 4.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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24570 28677: contig of 4108 bp in length
28678 28777: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1137 1236: gap of 100 bp 1237 2859: contig of 1623 bp in length
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human.
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ORGANISM
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AUTHORS
                                                                                                                                                                                                                                                      RESULT 3
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KEYWORDS
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                                                                   41824 41923: gap of 100 bp 41924 50252: contig of 8329 bp in length 50253 50352: gap of 100 bp 50336 60535: contig of 100 bp 60536 60535: contig of 100 bp 60536 60535: contig of 100 bp 60536 60535: gap of 100 bp 72137 72236: gap of 100 bp 72137 72236: gap of 100 bp 72237 87739: contig of 15503 bp in length 87740 87839: gap of 100 bp 102959: contig of 15503 bp in length 102960 103059: gap of 100 bp 103059: gap of 100 bp 103059: gap of 100 bp 121781 121880: gap of 100 bp 121880: gap of 100 b
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                    100 bp
of 7747 bp in length
100 bp
of 8329 bp in length
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/clone_lib="RPC1-11 Human Male BAC"
1. .1136
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121881. 149386
/note="assembly_fragment"
26017 c 25454 g 48389 t
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16765. .20769
/note="assembly_fragment"
20870. .24669
/note="assembly_fragment"
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/note="assembly_fragment"
41924. .50252
/note="assembly_fragment"
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'note="assembly_fragment"
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/note="assembly_fragment"
103060. .121780
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/note="assembly_fragment"
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'note="assembly_fragment"
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/note="assembly_fragment"
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note="assembly_fragment"
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/note="assembly_fragment"
7419. .9360
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/note="assembly_fragment"
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/note="assembly_fragment
clone_end:SP6
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/db_xref="taxon:9606"
/chromosome="4"
                                                 23: contig of 7 gap of 10 52: contig of 8
oţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                             gap of
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                       34076:
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ORIGIN
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Query Match

0.3%; Score 76; DB 71; Length 149386;
Best Local Similarity 100.0%; Pred. No. 5.9e-30;
Matches 76; Conservative 0; Mismatches 0; Indels 0;

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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 165605)
Mclay, K.
Homo sapiens chromosome 1 clone RP11-382DB, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Sequencing vector: plasmid; L08752; 100% of reads Consensus quality: 162959 bases at least Q40 Consensus quality: 167379 bases at least Q30 Consensus quality: 164239 bases at least Q30 Insert size: 164805; sum-of-contigs Insert size: 164805; sum-of-contigs Quality coverage: 5.92x in Q20 bases; sum-of-contigs coverage: 7.08x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74427 74591: gap of 100 bp 111 length 17492 103412: contig of 28821 bp in length 103413 103512: gap of 100 bp 103513 10352: contig of 4540 bp in length 10853 108152: gap of 100 bp 10853 108152: gap of 100 bp 129521 129520: contig of 4348 bp in length 129521 129520: gap of 100 bp 129521 133362: contig of 3742 bp in length 133363 133462: gap of 100 bp 100 bp 100 bp 133462: gap of 100 bp 100 bp 100 bp 133462: gap of 100 bp 100 bp 100 bp 100 bp 133462: gap of 100 bp 10
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                            12695 ctgacctcaggtgatc 12710
                                                                                                                                                                                                                                             16458 CTGACCTCAGGTGATC 16473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165605 bp
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Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 3% of reads
Sequencing vector: plasmid; L08752; 96% of reads
Sequencing vector: plasmid; L08752; 96% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 166910 bases at least Q40
Consensus quality: 166790 bases at least Q30
Consensus quality: 166576 bases at least Q30
Insert size: 169295; sum-of-contigs
Insert size: 16910; 4.2% error; agarose-fp
Quality coverage: 6.15x in Q20 bases; sum-of-contigs
coverage: 6.35x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is a runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2051 2150; gap of 100 bp 2051 bp in length 2051 2150; gap of 100 bp 2051 2150; gap of 11023 bp in length 13174 13773; gap of 1100 bp 3822 38213; gap of 100 bp 38322 38321; gap of 100 bp 38322 38321; gap of 100 bp 38322 38321; gap of 100 bp 78430 94546; contig of 40008 bp in length 7830 78429; gap of 100 bp 78430 94546; contig of 16117 bp in length 94647 102356; contig of 7710 bp in length 102357 102456; gap of 100 bp 100 bp 102357 102456; gap of 100 bp 100 bp 102357 102456; gap of 100 bp 100 bp
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/note="assembly_fragment:03071"
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fragment_chain:2"
102457. 108098
/note="assembly_fragment:01472
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/note="assembly_fragment:01613
                                                       Web Site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                  Summary Statistics
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                      Center project name: bA517124
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      Center: Sanger Centre
                                    code: SC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 170195)
Burton,J.
Direct Submission
Submitsed (19-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries; humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jan 21, 2001 this sequence version replaced gi:12227373.
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*** SEQUENCING IN
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                        vector_side:left"
40148 .54951
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fragment_chain:1"
55052 . .65031
/note="assembly_fragment:02156
fragment_chain:1"
65132 . .74491
/note="assembly_fragment:03743
fragment_chain:1"
74592 . .103412
/note="assembly_fragment:01859
fragment_chain:1"
74592 . .103412
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1. .40047
/note="assembly_fragment:01339
fragment_chain:1
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/note="assembly_fragment:02367
fragment_chain:2"
108153. .129520
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/note="assembly_fragment:00821
fragment_chain:3"
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fragment_chain:3"
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33042 c 32203 g 45392 t
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100.0%; Pred. No. 6e-
ive 0; Mismatches
/organism="Homo sapiens'
/db_xref="taxon:9606"
                                                                                     /clone="RP11-382D8"
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Best Local Similarity 100.0
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AL357556/c
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  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-NOV-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerquest@sanger.ac.uk
On Sep 30, 1998 this sequence version replaced gi:3646060.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence is the entire insert of clone 281H8. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HS281H8 110414 bp DNA PRI 23-NOV-1999
Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3.
Contains up to four novel genes, one with similarity to KIAA0323
and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3
(the latter in an introm of a novel gene). Contains ESTs, STSs,
GSSs, a putative CpG island and genomic marker D6S1553, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DA 162512 TTTTTTGAGACGGAGTTTCACTCTTGTTGCCCAGGCTGGAGTGCAATGCGCGTGATCTC 162453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human chromosome 6, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 5281H8 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALO31133.1 GI:3676189
HTG; C30F12.1; CpG island; D6S1553; KIAA0323; SMT3; Ubiquitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                 108199, .125531
//note~assembly_fragment:00163
/fragment_chain:2"
125632, .145739
//note~assembly_fragment:01151
/fragment_chain:2"
145840, .170195
                                                                                                                                                                                                                                                                                                                                                                                 DB 80;
6e-30;
                                                                                                                                                                                    /note="assembly_fragment:02163
fragment_chain:2
clone_end:T7
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37221 c 36147 g 46669 t
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Pred. No.
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100.0%; Pred
0; }
fragment_chain:2"
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Mashreghi-Mohammadi, M.
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KEYWORDS
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2041. .1156

/note="AluJo repeat: matches 1. .116 of consensus"

2157. .2463

2494. .3534

/note="Match: ESTS T61230 AA811212 A1085416 T61116

AA089549 AAA28247 W07118 AA493141 A1148021 AA465621 A1142307

AA578894 AA327805 AA096262 AA133846 AA843407 AI148678

T48328 AI188279 AI201880 AA265594 T48329 AA255682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3538. 3735. 7735. 7735. 7736. 7004e-"Aludo repeat: matches 105. 305 of consensus" 3738. 3978 3979. 4290 7004e-"MLTIC repeat: matches 173. 400 of consensus" 7004e-"Alusq repeat: matches 3. 299 of consensus" 4291. 4454 7004e-"MLTIC repeat: matches 6. 173 of consensus" 7004e-"MIR repeat: matches 19. 233 of consensus" 7004e-"MIR repeat: matches 19. 233 of consensus" 5184. 5461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5184. 5461

/note-"AluJo repeat: matches 5. 303 of consensus"

5480. 5757

/note-"LJMB3 repeat: matches 5290. 5592 of consensus"

6256. 6532

/note-"AluSg repeat: matches 1. 294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9503. .9582
/note="1.1M2 repeat: matches -493. .-427 of consensus"
10792. .10933
/note="1.11931 repeat: matches 5687. .5828 of consensus"
10935. .11153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6185 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296. .598
/note="*llusg repeat: matches 1. .294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anote="Alusg repeat: matches 1. .309 of consensus" 8451. .8745
Anote="Alusb repeat: matches 1. .299 of consensus" 8877. .8849
Anote="MIR repeat: matches 31. .104 of consensus" complement(9239. .9391)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="AluJo repeat: matches 1. .216 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 32. .152 of consensus" 12976. .13062
                                                                                                                                                                        .62 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      partially supported by FGENES and GENSCAN"
/evidence=not_experimental
/product="d1281H8.1 (PUTATIVE novel proteil join(11655...11734,20172...20399)
/gene="d1281H8.1"
/11878...11988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(<11655. .11734,20172. .>20399)
/gene="dJ281H8.1"
                                                                                                                                                                                                                                             1982. .2036
/note="MLT1B repeat: matches 336.
                                                                                                                                                                        'note="AluS repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                matches
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/note="match: STS G02971"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: ESTs R16664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3150, .3521)
/note="match: STS G41905"
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11158. .11474
/note="L1MB3 repeat:
                                                                    /map="q25.1-25.3"
/clone="RP1-281H8"
/clone_lib="RPCI-1"
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/note="1.12" repeat: matches 3. .311 of consensus"
14304. .14507
/note="1.1PA15 repeat: matches 5774. .5985 of consensus"
14710. .14951
/note="1.2 repeat: matches 1763. .2029 of consensus"
14952. .15082
                                                                                                                                                                                                                                                                                                                                                                                                  /note="L2 repeat: matches 2124. .2383 of consensus" 16167. .16599 /note="Charlielb repeat: matches 74. .511 of consensus" 16600. .16897 /note="Alusg repeat: matches 1. .299 of consensus"
                                                                                        -416. .-78 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16898. 16981
/note="charlielb repeat: matches 1. 74 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // Note="MillB repeat: matches 7. .376 of consensus" complement(19861. 20234)
200624. .20842
/ Note="Match: GSS AQ199235"
/ Note="MIR repeat: matches 14. .261 of consensus" / Note="MLTID repeat: matches 249. .359 of consensus" 23854. .24062
23664. .24062
24066. .24114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 59. .110 of consensus" 2428. .24407
/note="Alusc repeat: matches 124. .303 of consensus" 24409. .24405
/note="Alusx repeat: matches 3. .301 of consensus" 24744. .24807
/note="Miss repeat: matches 56. .121 of consensus" 25312. .25609
                                                                                                                                                                                                                                                                "note="FLAM_A repeat: matches 4. .132 of consensus"
5219. .15388
                                                                                                                                                                                                                                                                                                       /note="12 repeat: matches 2382. .2551 of consensus" 15389. .15705 /note="AluJo repeat: matches 3. .312 of consensus" 15706. .15934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L2 repeat: matches 1206. .1570 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2710 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           // note="AluSx repeat: matches 1. .298 of consensus" 26509 .26813 // note="AluSp repeat: matches 5. .310 of consensus" 26754 ..27134 // note="match: EST AA731910" // note="match: EST AA731910"
                                         note="Alusx repeat: matches 1. .298 of consensus"
13589. .13906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .288 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluSp repeat: matches 1. .295 of consensus"
19529. .19847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .298 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .293 of consensus"
'note""MIR repeat: matches 65. .167 of consensus"
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30073. .30348
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17972. .18259
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18269. .18560
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27880. .28189
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19058. .19349
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27232. .27530
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29416. .29709
                                                                                      /note="L1M3e repeat: matches 14021. .14300
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Direct Submission

L Submitted (09-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Dec 4, 2000 this sequence version replaced gi:9795179.

During sequence assembly data is comparad from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Ems., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP Information on the WORWPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human decreases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is the entire insert of clone RP1-28F12 The true left end of clone RP5-1076E17 is at 58615 in this sequence. The true right end of clone RP1-12201 is at 2837 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least
                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HS28F12 120630 bp DNA PRI 18-MAR-2001
Human DNA sequence from clone RP1-28F12 on chromosome 20411.22-12
Contains part of the KIAA0823 gene, ESTs, STSs and GSSs, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 120630)
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Pieter de Jonn. For the Information can be found at http://www.sanger.ac.uk/HGP/Chr20
Pieter de Jonn. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                          .2046 of consensus"
                                                                                                                              .2109 of consensus"
                                                                                                                                                                                                       32383. .32693 **
7note-"Alusx repeat: matches 1. .311 of consensus"
join 532815. .32954,37885. .38119,42063. .42169)
/gene-"adu281H8.2
                                                                                                                                                                               .552 of consensus"
                                                                              .271 of consensus"
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                                                                                                                                                                                                                                                                                                                                   Length 110414;
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                     /note="L2 repeat: matches 1449.
31086. 31356
/note="AluSg repeat: matches 1.
                                                                                                 31357. 31424
/note="L2 repeat: matches 2046.
31718. 32264
/note="MLT2D repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                      Score 75; DB 92;
Pred. No. 2.1e-29;
                                                                                                                                                                                                                                                                                                                      0.3%; Scc. 100.0%; Pred. No. 2... 0; Mismatches ...
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HTG; KIAA0823.
.31085
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Best Local Similarity 100.v
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KEYWORDS
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7041. 3166

// hote="Alusg/x repeat: matches 182. 3790 of consensus"
1041. 3532

// hote="Alusg/x repeat: matches 182. 308 of consensus"
10541. 3532

// hote="Alusg/x repeat: matches 1. 311 of consensus"
// hote="match: 328. 3626)

// hote="match: GSS: Em:AQ493285"
// hote="match: GSS: Em:AQ493295"
// hote="match: GSS: Em:B63323"
// hote="match: GSS: Em:AQ610322"
// hote="match: GSS: Em:AQ610322"
                                                                                                                                                                                                                                                                                                                                                                            2446. .2705
/note="AluSx repeat: matches 53. .311 of consensus"
2726. .3021
/note="LIMC/D repeat: matches 5495. .5796 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6904. .7215
/note="AluJo repeat: matches 1. .303 of consensus"
7227. .7540
/note="AluJo repeat: matches 1. .310 of consensus"
8181. .8349
/note="LIMD2 repeat: matches 5667. .5831 of consensus"
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hote="L1MC5 repeat: matches 7522. .7931 of consensus"
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note="FLAM_A repeat: matches 19. .110 of consensus"
1808. .6112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309. .4643
note="AluSx repeat: matches 7. .312 of consensus"
one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Location/Qualifiers
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note="Alusx repeat: matches 1. .301 of consensus"
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11233. .11520
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                                                                                                                                                                                                                                                                                                                          .282 of
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/note="LTR33 repeat: matches 41.
4160. .4308
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/note="AluSq repeat: matches 1.
complement(2169. 2835)
/note="match: GSS: Em:AQ342910"
                                                                                                                                                                                                     /note="Aluy repeat: matches 2.785.1139"
/note="match: GSS: Em:AQ770843"
complement (817.1337)
                                                      1. .120630
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
/map="q11.22-12"
                                                                                                                                                  /clone="RP1-28F12"
/clone_lib="RPCI-1"
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                                       FEATURES
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/note="MLTIB repeat: matches 115. .390 of consensus"
16731. .17043
/note="MLTIB repeat: matches 1. .312 of consensus"
17044. .17159
/note="MLTIB repeat: matches 1. .115 of consensus"
17160. .17378
/note="LZ repeat: matches 2376. .2584 of consensus"
17594. .17605
/note="MERSA repeat: matches 150. .161 of consensus"
1706. .17728
/note="LMC4 repeat: matches 7854. .7977 of consensus"
1777. .1723 repeat: matches 7071. .7608 of consensus" //octe="MLTIF repeat: matches 238. .288 of consensus"
//octe="MLTIF repeat: matches 374. .529 of consensus"
//octe="MLTIF repeat: matches 374. .529 of consensus"
//octe="MLTIF repeat: matches 1. .149 of consensus"
//octe="MEMEMC repeat: matches 1. .149 of consensus"
//octe="MEMEMC repeat: matches 1. .149 of consensus" /note="Alujo repeat: matches 148. .309 of consensus" 16351. .16459 /note="L2 repeat: matches 2584. .2685 of consensus" 16460. .16730 Anote-"Alujo repeat: matches 141. .302 of consensus" 18512. .19040 .276 of consensus" repeat: matches 97. .390 of consensus" Anote="AluJo repeat: matches 1. .141 of consensus" 17924. .18228 Anote="AluY repeat: matches 1. .305 of consensus" 18229. .18372 /note="Alux repeat: matches 1. .311 of consensus" 19463. .19495 'note="MER5A repeat: matches 44. .79 of consensus" /note="MER5B repeat: matches 1. .106 of consensus" /note="MSTB repeat: matches 2. .422 of consensus" 20335. .20429 .276 of /note="34 copies 2 mer ct 66% conserved" 19152. .19462 211. repeat: matches 244. /note="MLTIF repeat: matches 11759. .11811 9081. .19148 note="L1MC4 repeat_region repeat_region

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44
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DOE Joint Genome Institute.

DOE Joint Genome Institute.

Submitsted (03-4405-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 37 (Dass 1 to 142515)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142515)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-JUL-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 28, 2000 this sequence version replaced gi:7711297. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                     90971 CIGGTCTCGAACTCCTGACCTCAGGTGATCCACCCCCACCTCCAGCCTTCCCAAAGTGTTGGGA 91030
                                                                                                                                                                                                                                                Qy 17559 ctggtctcgaactcctgacctcaggtgatccacccacctcagcctcccaaagtgttggga 17618
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRI 28-JUL-2000 Homo sapiens chromosome 19 clone CTC-526N19, complete sequence. AC008556
                                                                                                                                                                                                                 Gaps
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                                                   .306 of consensus"
                                                                                     .303 of consensus"
                .304 of consensus"
                                                                                                                      /note="AluY repeat: matches 1. .294 of consensus'
22697. .23131
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Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                             Indels
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Estimated Total Number of Errors is 0.6.
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2.1e-29;
hes 0;
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Best Local Similarity 100.0%; Pred. No. 2.1e-29;
Matches 75; Conservative 0; Mismatches 0;
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21657. .21946
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                                                                                                                                                                        0.3%; Score 75; DB 100.0%; Pred. No. 2.1 Live 0; Mismatches
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a 33968 c 33523 g 38986
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1. .142515
/organism="Homo sapiens"
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                                 .21646
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                                                                                                                                                       Direct Submission
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20469
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8486 tggtgaaaccctgtctgtactaaaaatacaaaaattagctgggtgtggtggcgcatgcct 8545

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This clone was provided for sequencing by Dr. Stephen Scherer, Department of Genetics, The Hospital for Sick Childran, Toronto, Ontario, Canada with support from the Canadian Genome Analysis and Technology Program, and Dr. John D. McPherson, Department of Genetics, Mashington University, St. Louis MO. For additional information about the map position of this sequence, see http://www.genet.sickkids.on.ca/chromosome7 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-APR-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
3 (bases 1 to 155952)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (03-FEB-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                        ACO04534 155952 bp DNA PRI 03-FEB-2000
Homo sapiens PAC clone RP4-545C24 from 7q21-q22, complete sequence.
ACO04534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTICE: This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
Db 110391 TGGTGAAACCCTGTCTGTACTAAAAATACAAAAATTAGCTGGGGTGTGGGGCGCATGCCT 110450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ρλ
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The clone is available from Genome Systems, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dauphin, S. and Biewald, T.
The sequence of Homo sapiens PAC clone RP4-545C24
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.genomesystems.com).
VECTOR: pCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 155952)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 155952)
Waterston, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC004534.1 GI:3041858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WUGSC
                                                                                                                                             Db 110451 GTAATCCCAGCTACT 110465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE INFORMATION:
                                                                                                             8546 gtaatcccagctact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
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/translation="MGGFSRRCSKLINSSOLLYOEYSDVVLNKEIOSOORLESLSETP

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oin(22243. 22285,22477. 22730,26536. 26696,27252. 27404,7674. 27803,28058. 28132,28570. 28659,30107. 30264,0889. 31050,32495. 32565,34137. 34241,35274. 35431)
               The actual start of this clone is at base position 1 of RP4-545C24; actual end is at 155952 of RP4-545C24. The orientation of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note-"match to U02082 (PID:9484102); H_DJ0545C24.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="guanine nucleotide regulatory protein"
/protein_id="AAC12958.1"
/db_xref="GI:3041860"
                                                                               This clone contains STS SWSS1033 (NID:g1916393).
Location/Qualifiers
1. .155952
                                                                                                                                                                                                                                                                                                      501...1104
/rpt_family="MER4-group"
1173...1466
/rpt_family="Alu"
1469...1775
/rpt_family="Alu"
                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                     110. .413
/rpt_family="Alu"
414. .458
/rpt_family="(TAGA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9916. .10218
/rpt_family="alu"
14134. .14177
/rpt_family="(CA)n"
14789. .14837
14964. .15454
                                                                                                                                                                                   /map="7q21-q22"
/clone="RP4-545C24"
/clone_lib="RPCI-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="Alu"
5683. 5980
/rpt_family="Alu"
6081. 6171
/rpt_family="L2"
5855. 6641
/rpt_family="Alu"
6760. 7052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="MIR"
[1033. 1652]
[1053. 1562]
[1726_family="Alu"
[1726_ 17832
[7xpt_family="L2"
2224] 35431
[9ene="TIM"
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592. .7822
'rpt_family="MIR"
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/rpt_family="L2"
15478. .15762
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rpt_family="Alu"
907. .5226
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/rpt_family="Alu"
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5784. .15832
                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="Alu"
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540. .4841
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rpt_family="L2"
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                                                 clone is unknown
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27249. .27424
/gene="TIM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match to EST AA203715 (NID:g1799442) zx52f10.r1"
30889. .31056
/gene="TIM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match to EST AA059348 (NID:91553172) zf65f11.rl" 27667. .27803 /gene="TIM"
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4301. .34580
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35255. 33454
/note="match to EST AA203715 (NID:g1799442) zx52f10.rl"
36892. 37016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match to EST AA059348 (NID:g1553172) zf65f11.rl" 28568. .28659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match to EST AA059348 (NID:g1553172) zf65f11.rl" 29220. .29513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match to EST AA059348 (NID:g1553172) zf65f11.rl" 30173. .30265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match to EST AA203715 (NID:91799442) zx52f10.rl" 32490. .32565
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Best Local Similarity 100.0%; Pred. No. 2.2e-29;
Matches 75; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="Alu"
26157. 26281
26435. 26499
26456. 26698
/gene="TIM"
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30102. .30153
/gene="TIM"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="MIR"
24825. .24853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alu"
34890. .35071
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                                                                                                                                                                                                                                                                                                                                    /rpt_family="Alu"
23900. .24050
                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="MIR"
24526. .24637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="7SK"
24990. .25276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="Alu"
25845. .26140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="L2"
25344. .25647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .25647
                                                                                                                                                                                                                                                                                                     23752
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23447. .237
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Jayles. .113423

Jayles. .113423

Jayles. .113423

Jayles. .113423

Jayles. .14154

/note="Lilme1 repeat: matches 610. .3 of consensus"

Jayles. .14134

/note="Lilme1 repeat: matches 5390. .5167 of consensus"

Jayles. .14414

/note="LilmA4 repeat: matches 742. .905 of consensus"

Jayles. .14608

/note="Filam_A repeat: matches 1. .126 of consensus"

Jayles. .14608

/note="Lilma4 repeat: matches 930. .1042 of consensus"

Jayles. .15816

/note="Lilma4 repeat: matches 294. .1 of consensus"

John - Illes - Ill
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1668. .16953
Anote="ALUX repeat: matches 1. .295 of consensus"
17125. .17538
Anote="match: multiple ESTs; low % ID; match: T59663
F0237 N35317; match: R10942 N73317 N20948 R38018 R42572;
match: R62472 R43248 R41198 R38482 R42487; match: R62572 N3737 N20948 R38018 R42572;
                                                                                                                                                                 4120. 4429

/ Anote="AluJb repeat: matches 3. 302 of consensus"
4561. 5055

/ Anote="LiMB0 repeat: matches 69. 572 of consensus"
5056. 5186

/ Anote="FIZAM_C repeat: matches 1. .132 of consensus"
5188. 5500

/ Anote="LiMB0 repeat: matches 567. 923 of consensus"
6890. 7101

/ Anote="Mirk repeat: matches 15. .228 of consensus"
7430. 7715

/ Anote="AluJb repeat: matches 1. .292 of consensus"
7718. 8028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9635. 9799
/note="Lina5A repeat: matches 636. .472 of consensus"
9700. .9814
/note="Lina15 repeat: matches 600. .458 of consensus"
11277. .1.1857
/note="Lina5"
12059. .12316
/note="Their repeat: matches 311. .902 of consensus"
12059. .12570
/note="Their repeat: matches 371. .121 of consensus"
12476. .12570
/note="AluJo repeat: matches 301. .107 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Incomplete repeat."
[2673. .12959
[note="AluSq repeat: matches 286. .1 of consensus"
[2968. .13106
[1046="FLAM.C repeat: matches 133. .2 of consensus"
[3148. .13425
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                                                                                                                                            .76 of consensus"
                                                        .282 of
                          3558. .3838 .
/note="AluSq repeat: matches 1.
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repeat: matches 4982.
                                                                                                              1035. .4117 '
/note="LIME3 repeat: matches
                                                                                      incomplete repeat"
4035, .4117
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/note="AluJ repeat: matches 1. .55 of consensus; incomplete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The true left end of clone 26H23 is at 1 in this sequence. The true right end of clone 130N4 is at 34585.
The true left end of clone 267P19 is at 91732.
26H23 is from the human PAC library described in Ioannou A.P. et al Nature Genet 6, 84-89.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is not the entire insert of clone 26H23. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence has been finished according to sequence map criteria
                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                               Human DNA sequence from PAC 26H23, BRCA2 gene region chromosome 13q12-13 contains ESTs, CpG island. 284467 285990 285991 285992 285993 284467.1 GI:2104578 human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-MAY-1997) Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, UK. B-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 17, 1997 this sequence version replaced gi:1806009. IMPORTANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3346. .3416 -
/note="LiMB4 repeat: matches 859. .929 of consensus"
3418. .3552
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//note="Alusq repeat: matches 3. .303 of consensus"

//note="MSTD repeat: matches """

1669. 1796
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/note="LlMB4 repeat: matches 2. .91 of consensus"
817. .1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84. .1 of consensus;
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/note="MSTB repeat: matches 289.
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note="L1 repeat: matches 4886.
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/note="AluSc repeat: matches
incomplete repeat"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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/note="L1MA4 repeat:
1195. .1249
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/clone_lib="RPCI-1"
/clone="XX-26H23"
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Williamson, H.
                          Db 140907 CCTCTGCCTCCCAGG 140921
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/note="THEIC repeat: matches 371. 316 of consensus" 22624. 22654 ... 22950 /note="Math repeat: matches 372. .1 of consensus" 23311. .2361 /note="Alusg repeat: matches 299. .3 of consensus" 23864. .24165 /note="Alusg repeat: matches 303. .1 of consensus" 24267. .24562 /note="Alusg repeat: matches 4. .299 of consensus" 24562. /note="Alusg repeat: matches 4. .299 of consensus" 24559. .24604 /note="single clone" 24931. .25227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    incomplete repeat.
2554. .26134
/note="Libration and the second and the second and secon
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27019. .27146
/note="L1 repeat: matches 5022. .4893 of consensus"
27316. .27534
/note="AluJb repeat: matches 302. .85 of consensus;
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25424. .25562
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/note="THELC repeat: matches 1. .371 of consensus"
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                                90 % conserved"
                     15 copies of 2 mer .22555
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27720. .27880
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Direct Submission

Submitted (26-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerquest@sanger.ac.uk

On Dec 3, 1999 this sequence version replaced gi:6522765.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, RBML; Sw.; SWISSROT; Tr:, TREMBL; Wp.; WORNPEP; Information on the WORNEP database can be found at their source databases:

on the WORNEP database can be found at the from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20

Mapping Group. Further information can be found at the proposer ac.uk/MGY/Chr20

This sequence is the entire insert of clone RP4-800C24 The true left end of clone RP11-195M11 is at 77455 in this sequence. This sequence is the entire insert of clone RP4-800C24 The true left end of clone RP11-195M11 is at 37455 in this sequence. This sequence is the entire insert of clone RP4-800C34 as lone as compressions and repeats; all regions were enther double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as sometime with a sequence than one M13 subclone; and the assembly was confirmed by restriction digest. RP4-800C24 is from further than all the double or more than one M13 subclone; and the assembly was confirmed by the group of Pieter de Jong. For firther details and repeats. HSJ800C24 118150 bp DNA PRI 01-MAR-2001 Human DNA sequence from clone RP4-800C24 on chromosome 20 Contains an RPL12 (60S ribosomal protein L12) pseudogene, ESTs, STSs and Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 118150) /note="L1M4 repeat: matches 5194. .5658 of consensus" 3150. .3246
/note="AluSc repeat: matches 19. .123 of consensus"
3247. .366// Anote="MER66-internal repeat: matches 4687. .5105 of consensus" 1157. .1583 /note="MER66A repeat: matches 27. .438 of consensus" 1595. 3146 /note="MER66-internal repeat: matches 5118. 6676 of .749 of consensus" /note="match: STS: Em:HSPF12E2 Em:294572" /note="MER63 repeat: matches 3. 547. .995 further details see
http://www.chori.org/bacpac/home.htm /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="20" /clone="RP4-800C24" AL121593.10 GI:6523758 HTG; ribosomal protein; RPL12. Location/Qualifiers /clone_lib="RPCI-4" 9. .319 GSSs, complete sequence AL121593 1. .118150 Blakey, S. Direct Submission 76. .194 pCYPAC2. repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region misc_feature DEFINITION ACCESSION VERSION KEYWORDS ORGANISM RESULT 46 HSJ800C24 JOURNAL REFERENCE FEATURES TITLE COMMENT SOURCE

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/note="L2 repeat: matches 2372. .2412 of consensus"
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Moote="HUERS-P3 repeat: matches 4401. .4713 of consensus"

7459. .6893

Anote="HERV9 repeat: matches 3301. .4184 of consensus"
                                                                               /note="LIME1 repeat: matches 5521, .6073 of consensus"
23214, .23728
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Mote="THEIA repeat: matches 1. .354 of consensus"
16725. 16844

17022. 17319

Mote="Alusc repeat: matches 1. .303 of consensus"
17022. 17319

Mote="1731"

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Anote="12 repeat: matches 1421. .2750 of consensus" 21150. .21305
Anote="LiMa repeat: matches 3691. .3855 of consensus" 21297. .21820
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24228. .24266
                                                                                                                                                                                                                                                                 consensus"
9228. .9442
/note="MER66-internal repeat: matches 2887. .3102 of
                               1076. 4216
/note="MER66-internal repeat: matches 4548. .4688 of
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'note="MER66-internal repeat: matches 1210. .2844 of
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note="MER66A repeat: matches 29. .438 of consensus"
.1423. .11709
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// 17917. .1835/
// Anote="match: GSS: Em:B47157"
// Anote="MIR repeat: matches 1. .145 of consensus"
// B1589. .1907/
// Anote="MSTA repeat: matches 1. .426 of consensus"
// Anote="MSTA repeat: matches 1. .426 of consensus"
/note="MSTA repeat: matches 1. .426 of consensus"
1076. .4216
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9466. .10403
/note="MER66-internal repeat: matches 115. .1114
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/note="THEIA-internal repeat: matches 1. .1580 of
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"note="MER83-internal repeat: matches 1907.
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                                                                                                                                                                                                                      // note="Milks repeat: matches 1. .318 of consensus" 25399. 25601 // note="Milks repeat: matches 1. .189 of consensus" 25399. 25601 // note="Milk repeat: matches 45. .147 of consensus" 27171. 27202 // note="Milk repeat: matches 45. .147 of consensus" 27171. 27202 // note="Milk repeat: matches 284. .567 of consensus" 28399. 28390 // 2856 // note="Milk repeat: matches 10. .187 of consensus" 28398. 2856 // note="Milk repeat: matches 1. .164 of consensus" 28398. 2856 // note="match: 685: Em:AQ590436" // note="match: 685: Em:AQ590436" // note="match: 685: Em:AQ590436" // note="match: 7855 // note="matches 49. .260 of consensus" // note="9.29742 // note="matches 1. .308 of consensus" // note="matches 1. .308 of consensus" // note="matches 1. .308 of consensus" // note="matches 1. .294 of conse
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match: cDNAs: Em:L04479 Em:X53504 Em:AF037643 Em:D28443
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/note="dJ800C24.1 (RPL12 (60S ribosomal protein L12)
                                                                                                                                                                                     'note="AluYb8 repeat: matches 1. .318 of consensus"
                                                            .2494 of consensus"
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lilarity 100.0%; Pred. No. 7.6e-29;
Conservative 0; Mismatches 0;
24351. .24466
/note="L2 repeat: matches 2388.
24972. .25284
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48612. .49108
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48612. .4910A
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8589. 8639

Anote-"MIR repeat: matches 63. .113 of consensus"

9150. .9158

/note-"clone 330012; gtttttttt in this entry; insertion"

/replace-"gt"

9151. .9450

/note-"27 copies 2 mer gt 87% conserved"

9533. .9586

/note-"27 copies 2 mer gt 87% conserved"

9825. .9956

/note-"MIR repeat: matches 35. .144 of consensus"

10001. .10183
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// note="MLT2FB repeat: matches 263. .414 of consensus"
16256. .16405
// note="MIR repeat: matches 32. .173 of consensus"
16506. .16582
// note="MIR repeat: matches 185. .262 of consensus"
16603. .16675
// note="MIII repeat: matches 61. .135 of consensus"
complement(<17679. .>18271)
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note="MER74A repeat: matches 476. .531 of consensus"
819. .8126
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19875. .20175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7819, .8126
//note="AluSq repeat: matches 1. .308 of consensus" 8127, .8585
/note="MER74A repeat: matches 3. .476 of consensus" 8589, .8639
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                                 .2691 of consensus"
                                                                                                                             /note="AluJb repeat: matches 1. .296 of consensus" 12245. .12322 /note="MIR repeat: matches 127. .214 of consensus" 14029. .14111
                                                                                                                                                                                                                                                                                                                                                                                 687. 6817
fnote="MIR repeat: matches 122. .247 of consensus"
7526. 7653
rocte="MIR repeat: matches 54. .170 of consensus"
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                                                                                                                                                                                                                                                                                                                                                       .138 of consensus"
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                                                                                                   .100 of consensus"
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Thote="MIR repeat: matches 63. .262 of consensus" 11827. .11941
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                                                                                                                                                                                                                                                                                               6243. .6272
/note="MIR repeat: matches 109.
6687. .6817
                                       repeat: matches 2488.
                                       462. 4714
/note="MIR repeat: matches 48.
5433. 5469
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11942. .12244
4373. .4578
/note="L2 rer
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                                                                                                                                                                                                                                                                                                                                                                           Direct Submission

The Paragola Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

requests: clonerequest@sanger.ac.uk

on Jun 19, 1999 this sequence version replaced gi:4582139.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence has been finished according to sequence map criteria

as follows. An attempt is made to resolve all sequencing problems,

such as compressions and repeats, but not necessarily within known

annotated human repeat sequence elements (e.g. Alu). Where the

feature of the contraction using the 'unsure'

feature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chhl 69M21 is from the library RPC11 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2 This sequence is the entire insert of clone 69M21. The true right end of clone 330012 is at 31830 in this sequence.
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                    DNA PRI 23-NOV-1999 clone 69M21 on chromosome 1p36.21-36.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .391. .3556
'note="MER69 repeat: matches 2137. .2318 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1206. 3380
(note="AluJb repeat: matches 131. .294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note-"MER69 repeat: matches 718. .763 of consensus"
2265. .2556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MLT1D repeat: matches 169, .505 of consensus"
2557, .2855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note-"MER69 repeat: matches 763. .867 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .198 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L2 repeat: matches 2358. .2488 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="AluSx repeat: matches 21. .237 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           616. .914
/note="AluSx repeat: matches 1. .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      557. .2855
note="AluSx repeat: matches 1. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1856. 3036 ..... matches 1. .169 of consensus" MLTID repeat: matches 1. .169 of consensus" 1037. .3162
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/note="AluSq repeat: matches 1. .299 of consensus"
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                                                                                                   complete sequence.
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note="MER69 repeat: matches 37.
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/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="p36.21-36.23"
/clone="RP1-69M21"
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         125937 bp During from c
                                              Human DNA sequence from Contains ESTs and GSSs, AL031735
                                                                                                                                                           AL031735.9 GI:5102570
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 135252)
                                                                                                                                                                                                                                                                  Submitted (21-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jan 5, 2001 this sequence version replaced gi:12001719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 134152; sum-of-contigs
Insert size: 145141; 4.6% error; agarose-fp
Quality coverage: 6.06x in Q20 bases; sum-of-contigs Quality
coverage: 5.85x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently
consists of 12 contigs. The true order of the pieces
is not known and their order in this sequence record is
runs of whit the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
so so no sit is available and the accession number will
be preserved.
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117665 119820: contig of 2156 bp in length
119821 119920: gap of 100 bp
119921 135252: contig of 15332 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasembly program: XGAP4, version 4.5
Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 130150 bases at least Q40 Consensus quality: 131436 bases at least Q30 consensus quality: 132572 bases at least Q30
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76714 79317: contig of 2604 bp in length
79318 79417: gap of 100 bp
79418 103390: contig of 23973 bp in length
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                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. 135252
7.organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
  PROGRESS ***, 12 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="1"
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/clone_lib="RPCI-4"
1. .17724
                                                   GI:12043508
                                                                                                                                                                                                                                                                                                                                                                                                 Center: Sanger Centre
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                                                                                                                          Homo sapiens
                                                   AL512423.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                        23344. .22421
/note="LiMC5 repeat: matches 7163. .7239 of consensus"
22427. .22687
/note="MER20 repeat: matches 1. .218 of consensus"
22683. .22987
/note="AluJo repeat: matches 1. .135 of consensus"
22988. .23284
                                                                                                                /ncellace="fct" 2022.
2027. .20522
/note="Alusx repeat: matches 1. .299 of consensus" 20533. .20892
/note="Libes repeat: matches 5766. .6134 of consensus" 20899. .21186
                                                                                                                                                                                                                                                                    /note="AluJo repeat: matches 1. .301 of consensus" 21192. .21465
/note="L2 repeat: matches 2137. .2418 of consensus" 21542. .22135
/note="LiMC5 repeat: matches 7260. .7791 of consensus" 22136. .22294
                                                   matches 6134. .6172 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                      .308 of consensus"
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Homo sapieņs chromosome 1 clone RP4-539L13, *** SEQUENCING IN
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70cte="L2 repeat: matches 2445. .2669 of consensus" 23905. .33940

70ote="MRR81 repeat: matches 29. .68 of consensus" 23941. .24238

70ote="AluSx repeat: matches 1. .298 of consensus" 24239. .24299

70ote="MRR81 repeat: matches 68. .114 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L2 repeat: matches 2704, .2746 of consensus" 24659, .24792
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note="L2 repeat: matches 2452. .2709 of consensus"
6052. .26349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26052. .26349
note="AluJb repeat: matches 12. .305 of consensus"
26843. .26880
'note="AluSg1 repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18067. .28136

Thote="MIR repeat: matches 61. .131 of consensus"

18210. .28305

Thote: MIR repeat: matches 50. .146 of consensus"

18493. .28607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="MIR repeat: matches 6. .134 of consensus" 5494. .25748
                                                                                         /note="clone 330012; ct in this entry; deletion"
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                                                                                                                                                                                                                                                                                                                                                                                                              'note="AluSc repeat: matches 150.
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29321. .29572
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/note="L1MB6 repeat:
20226. .20227
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LOCUS DEFINITION

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RESULT 4 AL512423

Matches

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COMMENT
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[E. [Obasa 1 to 155190]

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, E., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davida, M.L., Davis, C., David, R., Davida, M.L., Davis, C., Delaney, K.R., Delaney, K.R., Delaney, K.R., Delaney, K.R., Delaney, K.R., Delaney, C., Edwards, C., Edwards, C., Elhaj, C., Escotto, M., Falls, T., Ferrautz, D., Flaggi, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gaevara, W., Gunaratne, P., Hale, S.,
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Homo sapiens chromosome 3 clone RP11-129P2, WORKING DRAFT SEQUENCE,
16 unordered pieces.
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100.0%; Pred. No. 7.7e-29;
Live 0; Mismatches 0; Indels 0;
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                                                                     /note-"assembly_fragment:01567"
11921. .13522
/note-"assembly_fragment:02053"
a 33936 c 34166 g 32963 t 1:
/note="assembly_fragment:01329
fragment_chain:1
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HTG: HTGS_PHASE1; HTGS_DRAFT.
                                                       vector_side:left"
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Best Local Similarity 100.0
Matches 74; Conservative
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KEYWORDS
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Hemilton, K. Harris, C., Darris, K. Harth, K. Harth, K. Harrish, P. Hawsa, A., Bernandes, J. Harroneca, Darris, R. Harris, C., Judy, C.,
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McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Naylor, J., Norman, C.H., O'Connoi, T., O'Vonnoi, P., O'Neil, D., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, W., X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (20-FBB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 12, 2000 this sequence version replaced g1:7008900. All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 157000; agarose-fp
Insert size: 156557; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; agarose-fp
Quality coverage: 3.9 in Q20 bases; sum-of-contigs
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12452 14390: contig of 125.

14391 14490: gap of 100 bp

14491 17367: contig of 2877 bp in length

17368 17467: gap of 100 bp

17468 21354: contig of 3887 bp in length
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1356 1455: gap of 100 bp
1456 2614: contig of 1159 bp in length
2615 2714: gap of 100 bp
4731 4230: gap of 100 bp
4231 5925: contig of 1695 bp in length
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21355 21454: gap of 100 bp
21455 214095: contig of 2641 bp in length
24096 24195: gap of 100 bp
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                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai. Euthenia; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 159057)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Chases 1 to 159057)

E 2 (bases 1 to 159057)

E 3 (bases 1 to 159057)

E 4 (bases 1 to 159057)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bedar, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., DeWar, K., Dodge, S., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Howland, J.C., Illey, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levlne, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,
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AC023995/c
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us-09-434-382-28.oli.rge

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misc_feature
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AC021346/c
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                                                                                 60218 60317: gap of 100 bp
60318 68951: contig of 8634 bp in length
                                                                                                                     51: gap of 100 bp 75496: contig of 6445 bp in length
                                                                                                                                                      75596: gap of 100 bp
83324: contig of 7728 bp in length
44434: contig of 8619 bp in length
                   oof 100 bp
contig of 7564 bp in length
                                                     98: gap of 100 bp
60217: contig of 8019 bp in length
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29215. . 35715
//note="assembly_fragment"
35816. . 44434
//note="assembly_fragment"
44535. . 52098
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69052. .75496
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69052 75
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1. (Dases 1 to 170795)
2. (Dases 1 to 170795)
2. (Dases 1 to 170795)
3. (Dases 1 to 170795)
4. (Dases 1 to 170795)
5. (Dases 1 to 170795)
5. (Dases 1 to 170795)
5. (Dases 1 to 170796)
6. (Dases 1 to 170796)
7. (Dases 1 to 170796)
8. (Dases 1 to 170796)
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 170795)
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Best Local Similarity 100.0%; Pred. No. 7.9e-29;
Matches 74; Conservative 0; Mismatches 0;
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AC021346.3 GT:10045520
HTG: HTGS_PHASE1: HTGS_DRAFT.
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Web site: http://www-seq.wi.mit.edu
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AC022735/c
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                Insert size: 164000; agarose-fp
Insert size: 169695; sum-of-contigs
Quality coverage: 5.3 in Q20 bases; agarose-fp
Quality coverage: 5.1 in Q20 bases; sum-of-contigs
                                                                                                                      Center clone name: 24_K_15

Center clone name: 24_K_15

Sequencing vector: M13; W77815; 100% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 163380 bases at least Q40

Consensus quality: 166786 bases at least Q20

Consensus quality: 168687 bases at least Q20
                                   48018: gap of 100 bp 59010: contig of 10992 bp in length 59110: gap of 100 bp 101273: contig of 42163 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113914 114013: gap of 100 bp
114014 126871: contig of 12858 bp in length
126872 126971: gap of 100 bp
126972 160480: contig of 33509 bp in length
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37474 37573: gap of 100 bp
37574 38717: contig of 1144 bp in length
38718 38817: gap of 100 bp
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101374 113913: contig of 12540 bp in length
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43847: contig of 2379 bp in length
43947: gap of 100 bp
47918: contig of 3971 bp in length
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39840: contig of 1023 bp in length
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39941 41368: contig of 1428 bp in length
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43948 479
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38718 38817:
38818 398
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Uppublished

2 (bases I to 176731)

Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Baldwin, J., Barna, N., Beckerly, R.,

Boduslavkly, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

Choepel, Y., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,

Ferreira, P., FitzHugh, W., Forres, C., Gage, D., Galagan, J.,

Ferreira, P., FitzHugh, W., Forres, C., Gage, D., Galagan, J.,

Rowland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Landers, T., Lehoczky, J., Levine, R., Lieu, G., Locke, K.,

Macdonald, P., Marquis, N., Mebwan, P., McGurk, A., McKernan, K.,

Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,

Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,

Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,

Zimmer, A. and Zody, M.

Direct, Submission, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,

Direct, Submission, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,

Direct, Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACO22735 176731 bp DNA HTG 03-FEB-2001
Homo sapiens chromosome 15 clone RP11-519P13 map 15, WORKING DRAFT
SEQUENCE, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 3, 2001 this sequence version replaced gi:7249212.

All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 66; Length 170795; 8e-29;
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                                                                                                                                                                                                                                                                                                                                                                    1105 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 176731)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone RP11-519P13
Unpublished
                                                                                                                                                                                                                                                                                                                                  vector_side:right" 54926 a 33714 c 33988 g 47062 t
                                                                                            Query Match 0.3%; Score 74; DB Best Local Similarity 100.0%; Pred. No. 8e-Matches 74; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smit, A.F.A. & Green, P. (1996-1997
/note="assembly_fragment"
101374. .113913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT
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Surren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Batren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Baldwin, J., Barna, N., Bastien, V., Beda, F., Baldwin, J., Barna, N., Burket, G., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Perreira, P., Fitzhudi, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gage, D., Grand-Pierre, N., Grank, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Lilev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Hein, J., LaRocque, K., Lamazares, R., Landers, T., Leboczky, J., Levine, R., Lieu, G., Locke, K., Macdonald, P., Maquis, N., McCerthy, M., McEwan, P., McGurk, A., Mickernan, K., McDheeters, R., Medrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., O'Donnor, T., O'Donnor, I., O'Donnor, I., O'Donnor, I., O'Donnor, I., O'Neall, D., Olivar, T.M., Olivez, J., Peterson, K., Peterson, K., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Tralamas, J., Voung, G., Zainoun, J., Zinmer, A. and Zody, M., Trigillo, J., Young, G., Zainoun, J., Zinmer, A. and Zody, M., Trigillo, J., Young, Submission
              Home sapiens chromosome 1 clone RP11-204L3 map 1, *** SEQUENCING IN PROGRESS ***, 81 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 14, 2000 this sequence version replaced gi:7770499.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 200484)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 81 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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contig of 1073 bp in length

p of 100 bp

contig of 1237 bp in length

p of 100 bp

contig of 1272 bp in length
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contig of 1322 bp in length
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                                                                                                                                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 1, clone RP11-204L3 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project Information Center project name: L7675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: 204_L_3
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1149 2470: cor
                                                                                                                                     AC025002.3 GI:8516086
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6352: r
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2571 3643:
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                                                                                                                                                                     HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                         Homo sapiens
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6453
7550
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                                                                                                                                                                                                  human.
                                                       DEFINITION
                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                           REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
  AC025002
                                                                                                                                                               KEYWORDS
                                                                                                                                        VERSION
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                                                                                                              Sequencing vector: M13; M7815; 57% of reads
Sequencing vector: M13; M77815; 57% of reads
Sequencing vector: Plasmid; n/a; 43% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 174754 bases at least Q40
Consensus quality: 175799 bases at least Q30
Consensus quality: 175799 bases at least Q30
Consensus quality: 175799 bases at least Q30
Insert size: 158000; agarose-fp
Insert size: 176331; sum-of-contigs
Quality coverage: 8.8 in RQ20 bases; agarose-fp
Quality coverage: 7.9 in Q20
* NOTE: This is a "working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105542 105641: gap of 100 bp 105542 105641: gap of 100 bp 105642 160623: contig of 54982 bp in length 160724 160724; contig of 16008 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    400 others
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2068 2167: gap of 100 bp
86428 86423: contig of 84256 bp in length
100 bp
86524 105541: contig of 19018 bp in length
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a 35801 c 34289 g 50265 t
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/note="assembly_fragment"
105642. .160623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2168. .86423
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                                                                              Center clone name: 519_P_13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP11-519P13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector_side:left"
                                                    Center project name:
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Best Local Similarity
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source

FEATURES

BASE COUNT ORIGIN

Matches

53

RESULT

99

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AC010553 85543 bp DNA PRI 28-JUN-2000
Homo sapiens chromosome 16 clone RP11-59D8, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 200484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103251: gap of 100 bp 100 bp 1005370: contig of 3119 bp in length 106470: gap of 100 bp 100888: contig of 2418 bp in length 108988: gap of 100 bp 111514: contig of 2526 bp in length 111614: gap of 100 bp 114460: gap of 100 bp 118260: contig of 3809 bp in length 118260: contig of 3809 bp in length 118260: contig of 3809 bp in length
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3537 bp in length
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3016 bp in length
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97163; contig of 2493 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 bp
3990 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 bp
3210 bp
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84126: contig of 2228 bp
84226: gap of 100 bp
86794: contig of 2568 bp
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3578 bp
 ďq
                                                                                                                       74635: Contig of 2128 bp
35: gap of 100 bp
77554: contig of 2819 bp
                                                                                                                                         p of 100 bp contig of 2819 bp
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80277: contig of 2623 bp
                                                                                                                                                                                                      177: gap of 100 bp
81798: contig of 1421 bp
198: gap of 100 bp
                                                                                                                                                                                                                                                                                                86894: gap of 100 bp
90311: contig of 3417 bp
                                                                                                                                                                                                                                                                                                                             90411: gap of 100 bp
92255: contig of 1844 bp
92355: gap of 100 bp
94570: contig of 2215 bp
                                                                                                                                                                                                                                                                                                                                                                                                                         :63: gap of 100 bp 99724: contig of 2461 bp
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contig of 4276 bp
                                                                             22: gap of 100 bp
72407: contig of 2185 bp
                                contig of 2480 bp
                                                              70122: contig of 1399 bp
66043: contig of 1500
43: gap of 100 br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1369: gap of
122359: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125669: contig of 3769: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1406: gap of
132984: contig of
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140476: contig of
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Human DNA sequence from clone RP11-374118 on chromosome 6, complete
sequence.
                                                                                                                                                                                                                                                       Direct Submission
Submitted (15-58P-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 85543)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (28-JUN-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jun 28, 2000 this sequence version replaced 91:8576035.
Draft Sequence Produced by DOE Joint Genome Institute
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157784)
Lawlor, S.
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 85543)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 14, 2001 this sequence version replaced gi:13396590.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.4% of Sequence;
Estimated Total Number of Errors is 0.5.
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19951 c 19917 g 22207 t
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/db_xref="taxon:9606"
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DOE Joint Genome Institute.
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AC010553.6 GI:8778952
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Unpublished
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 mapping the part of the constructed by the Sanger Centre Chromosome 6 mapping the construction can be found at the contraction can be found at t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGP/Chr6
RP11-374118 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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4595. .4630

4705. .4630

4705. .4927

4705. .4927

4705. .2780 of consensus"

5245. .5284

6066. .8377

Anote-"Li repeat: matches 2705. .2750 of consensus"

6706. .8377
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/clone_lib="RPCI-11.2"
2165. .2605
/note="MLTID repeat: matches 19. .501 of consensus"
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15273. .15540
/note="MER63B repeat: matches 1. .272 of consensus"
15926. .16160
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13252. .13442
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/note="62 copies 2 mer at 68% conserved" 8411. .8522

/note="8 copies 4 mer atat 70% conserved" 9401. .11199

/note="LIPA5 repeat: matches 4337. .6141 of con n 11887. .12021

/note="EIPA5 repeat: matches 81. .218 of conserved" 12705. .12795
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17433. .17598
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/db_xref="taxon:9606"
/chromosome="6"
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// Anote=""LRNA-GLy-GGC repeat: matches 1. .36 of consensus" 19417. 19822 / Anote="LLNA7 repeat: matches 5564. .6059 of consensus" 19821. .20173 repeat: matches 424. .865 of consensus" 21920. .22030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28581. .28624

/note="12 copies 2 mer ac 90% conserved"

28635. .28947

/note="LiMak repeat: matches 546%. .5782 of consensus"

31677. .31741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1MA4A repeat: matches 5802. .5912 of consensus"
                                                                               21920. .22030

//note="MIR repeat: matches 36. .147 of consensus"

22044. .23086

//note="LiPAy repeat: matches 4518. .5567 of consensus"

23087. .23637
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18140. .18446
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42093. .42398
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                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 40. .157 of consensus"
26873. .26155
/note="AluJo repeat: matches 1. .288 of consensus"
26575. .26610
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14475. .44692
                                      /note="AluY repeat: matches 1. .307 of consensus" 18733. .19120
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/note="18 copies 2 mer gt 91% conserved"
34230. .34261
/note="8 copies 4 mer tgtg 93% conserved"
35911. .35966
/note="14 copies 4 mer acac 91% conserved"
35917. .35966
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hote-"18 copies 2 mer aa 80% conserved"
26638. 26927
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41101. 41142
/note="MER69A repeat: matches 19. .168 or
41243. 41302
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16384)
S Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Coyle, M.D., Dathonne, S.R., David, R., Davila, M.L., Davis, C., Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
                                                                                        47127. 47397

Anote="AluJor repeat: matches 1. .277 of consensus"
A1398. 47460
Anote="21 copies 3 mer aat 84% conserved"
A1581. 47671
Anote="LIMA3 repeat: matches 35. .127 of consensus"
Anote="LIMA3 repeat: matches 6016. .6300 of consensus"
Anote="LIMA3 repeat: matches 6016. .6300 of consensus"
Anote="AluJb repeat: matches 1. .309 of consensus"
Anote="AluJb repeat: matches 1. .309 of consensus"
Anote="All Repeat: matches 38. .262 of consensus"
51938. .52144
Anote="MIR repeat: matches 247. .262 of consensus"
54096. .54112
Anote="LI repeat: matches 2649. .2690 of consensus"
Anote="MIR repeat: matches 173. .247 of consensus"
54153. .54181
Anote="MIR repeat: matches 5367. .6163 of consensus"
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                                                                     .303 of consensus'
                 /note="MIR repeat: matches 10. .255 of consensus" 4574. 46025
/note="AluJb repeat: matches 1. .303 of consensus 47127. .47397
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Local Similarity 100.0%; Pred. No. 2.9e-28;
les 73; Conservative 0; Mismatches 0;
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AC013245.18 GI:10445256
HTG; HTGS_PHASE1; HTGS_DRAFT.
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AUTHORS
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AC013245
LOCUS
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FEATURES
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C. Elbaj, C., Esoctuch, M., Falls, T.,
Enlaj, C., Esoctuch, M., Falls, T.,
Farstag, N., Ford, J.,
Gabis, A., Gao, J., Garcia, A., Garner, T.,
Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hales, S.,
Hamilton, K., Harris, C., Harris, K., Hatt, M., Havlak, P., Hawes, A.,
Hernandez, J., Hernandez, O., Hodgson, A., Hoglowa, C.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Jackson, L., Li, Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., Kuing, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Ludseged, H., Lozado, E., Eichtarge, C., Lieu, C., Liu, J., Liu, M.,
Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
Mayusen, A., Mayusen, R., Manier, S., Martin, R., Martindale, A.,
Martinez, E., Mawhiney, R., Miner, Z., Mitchell, T., Mohabbat, K.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N.,
Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Porce, A., Patce, M.,
Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,
Sisson, I., Sodergren, E., Sonaike, T., Zparks, A., Stanley, H.,
Tansey, J., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, S., Warlen, S., Warlingans, S., Warlen, S., Warlen
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ONDE: This is a "working draft' sequence. It currently
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-NOV-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 2, 2000 this sequence version replaced gi:10180134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length
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51194: gap of unknown length
89143: contig of 37949 bp in length
82143: gap of unknown length
123720: contig of 34477 bp in length
123820: gap of unknown length
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Contact: hgsc-help@bcm.tmc.edu
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123820:
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Unpublished
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Direct Submission
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51195
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TITLE
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COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 170970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy 18972 ggagatcgagaccatcctggctaacatgatgaaaccccgtctctactaaaaatacaaaaa 19031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (19-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Mar 24, 2001 this sequence version replaced gi:13398737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 170970 bases at least Q40
Consensus quality: 170970 bases at least Q20
Insert size: 170970; sum-of-contigs
Insert size: 176301; 3.8 error; agarose-fp
Quality coverage: 13.31x in Q20 bases; sum-of-contigs Quality
coverage: 13.30x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 9 clone RP11-390F4, *** SEQUENCING IN PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
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* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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143932: contig of 20112 bp in length
144032: gap of unknown length
153965: contig of 9933 bp in length
154065: gap of unknown length
162229: contig of 8164 bp in length
162329: gap of unknown length
163884: contig of 1555 bp in length.
                                                                                                                                                                                                                                                                                                 604 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                                1. .163884
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                          /clone="RP11-329010"
                                                                                                                                                           Location/Qualifiers
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                                               144033
153966
154066
162230
162330
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ORIGIN
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KEYWORDS
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Location/Qualifiers

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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4113. 4269
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/note="sequence from overlapping clone bA398019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (20-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Feb 21, 2001 this sequence version replaced gi:13016545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL445592 171173 bp DNA HTG 21-MAR-2001
Homo sapiens chromosome 9 clone RP11-660M15, *** SEQUENCING IN
PROGRESS ***, 14 unordered pieces.
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Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Consensus quality: 167022 bases at least Q40
Consensus quality: 168348 bases at least Q30
Consensus quality: 169150 bases at least Q20
Insert size: 169873; sum-of-contigs
Consensus coverage: 6.48x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.3%; Score 72; DB 89; I
100.0%; Pred. No. 1.1e-27;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                complement(125204, .12535)
/note="match: STS: Em:AU046368"
complement(12529, .125348)
/note="match: STS: Em:HSA108WE1"
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//note="match: STS: Em:C64211"
43014. .43323
/note="match: STS: Em:G05593"
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/note="match: STS: Em:G44152"
34936 c 34876 g 49028 t
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Web site: http://www.sanger.ac.uk
                         /organism="Homo sapiens"
                                                /db_xref="taxon:9606"
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AL445592.8 GI:13092319
HTG; HTGS_PHASE1; HTGS_DRAFT.
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Plumb, B.
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Matches 72; Conservative
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L Submitted (06-JAW-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. Email enquiries: humquery@sanger.ac.uk CB10 15A, UK. Email enquiries: humquery@sanger.ac.uk CB10 15A, UK. Email enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

on Jan 8, 2001 this sequence version replaced gi:11991348.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL138966 171160 bp DNA PRI 06-JAN-2001
Human DNA sequence from clone RP11-380N8 on chromosome 13, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Emm., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 171160)
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RP11-380N8 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
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                                                                                                                               /clone_lib="RPCI-11.2"
1. .170970
/note="assembly_fragment:03462
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VECTOR: pBACe3.6
                                                                                                                                                                                                                                  vector_side:right"
1 37367 c 38762 g 49705
                         /organism="Homo sapiens"
                                                /db_xref="taxon:9606"
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AL138966/c
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KEYWORDS
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COMMENT

FEATURES

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Length 171160; Indels

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NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7388 73888: gap of 73989 91570: contig of 17582 bp in length 91571 91670: gap of 100 bp 91671 104214: contig of 12544 bp in length 104315 104314: gap of 100 bp 118387 118486: contig of 14072 bp in length 118387 118486: gap of 100 bp 118487 138639: contig of 20153 bp in length 118487 138639: contig of 20153 bp in length
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138640 171173: contig of 32434 bp in length.
Location/Qualifiers
1. 171173
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                                                                                                                                                                                   1 2028: contig of 2028 bp in length
2029 2128: gap of 100 bp
2129 4271: contig of 2143 bp in length
4272 4371: gap of 100 bp
4372 6590: contig of 2219 bp in length
6591 6690: gap of 100 bp
6691 39312: contig of 32522 bp in length
9213 39312: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                               41360: contig of 2048 bp in length
60: gap of 100 bp
52781: contig of 11321 bp in length
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55092: contig of 2211 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92: gap of 100 bp 64599: contig of 9407 bp in length
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73888: contig of 9189 bp in length
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fragment_chain:2"
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73089. 104214
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4372. .6590
/note="assembly_fragment:03436
fragment_chain:1"
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vector_side:left"
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39313 4136
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41461 5278
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Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 13 clone RP11-309F17, *** SEQUENCING IN
PROGRESS ***, 5 unordered pieces.
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Submitted (07-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Mar 25, 2001 this sequence version replaced gi:13445987.
Center: Sanger Centre
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Insert size: 196815; 6.9% error; agarcae-fp
Quality coverage: 6.68x in 020 bases; sum-of-contigs Quality
coverage: 6.62x in 020 bases; agarcse-fp
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 192380 bases at least Q40
Consensus quality: 192954 bases at least Q30
Consensus quality: 193244 bases at least Q20
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1.1e-27;
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104315. 118386
/note="assembly_fragment:02124
fragment_chain:2"
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fragment_chain:2"
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fragment_chain:2"
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Web site: http://www.sanger.ac.uk
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 193830)
Mashreghi-Mohammadi,M.
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a 33865 c 37161 g
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Homo sapiens 12p13.3 RPCI4-773N5 (Roswell Park Cancer Institute
Human PAC library) complete sequence.
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                     MO 63108, USA
On Mar 22, 2001 this sequence version replaced gi:12740570
                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                          Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51: contig of 51 bp in length
151: gap of unknown length
12457: contig of 12306 bp in length
12557: app of unknown length
208248: contig of 195691 bp in length.
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152. .12457
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/organism="Homo sapiens"
                                                                               ----- Genome Center
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/clone="RP11-544H14"
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Matches 72; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Home sapiens chromosome UNK clone RP11-544H14, WORKING DRAFT SEQUENCE, 3 unordered pieces.
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Submitted (25-SEP-1999) Genome Sequencing Center, Washington
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                   87897 87966: gap of 100 bp 87997 137489: contig of 49493 bp in length 137490 137589 contig of 49493 bp in length 168075 168174: gap of 100 bp 168175 170782: contig of 2608 bp in length 170881 193830: contig of 22948 bp in length 170883 193830: contig of 22948 bp in length.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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1.1e-27;
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1. 87896
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18175. 170782
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168175. 170782
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57880 a 38659 c 38280 g 58611 t
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                                                                                                                                                                                                                           Location/Qualifiers
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Waterston, R.H.
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Waterston, R.H.
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AC010900/c
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AUTHORS
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KEYWORDS
SOURCE
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18435 . 18472
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19844 . 19869
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3214. .2350
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Location/Qualifiers
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4 (bases 1 to 57304)
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                                                                                Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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//note="Overlaps with AC004804 bases 108534 - 108879"
/function="Overlap with adjacent clone AC004804"
complement(802. .1201)
/note="Region: Similar to AA149366"
complement(891. .917)
/rpt_and_ny="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.
Direct Submission
Submitted (06-JUN-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 57304)
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/db_xref="taxon:9606"
/clone="RPC14-773N5"
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complement(2707. .2837)
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Direct Submission
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                                                        Homo sapiens
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Anderson, S., Barna, M., Bastlen, V., Bedar, F., Boquslarkiy, L.,
Burren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Barna, M., Bastlen, V., Bedar, F., Boquslarkiy, L.,
Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,
FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,
Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L.,
Illev, I., Johnson, R., Jones, C., Kanni, L., Karatas, A., Lieu, C., Liu, G.,
Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K.,
Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T.,
O'Donnell, P., O'Nell, D., Ollvar, T. W., Ollver, J., Peterson, K.,
Pierre, N., Pischman, D., Roy, A., Santos, R., Stolaner, S., Severy, P.,
Sougnez, C., Spencer, B., Stange-Thomann, N., Stolaner, S., Severy, P.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Travers, M., Trigillio, J., Vossiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Limmer, A. and Zody, M.
Direct Submission
Submitted (30-SEP-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2001 this sequence version replaced gi:10440690.
All repeats were identified using RepeatWasker:
Smit, A.F.A. & Green, P. (1996-1997)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web Site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: project Information
Center project name: L11229
Center clone name: 462_C_21
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                                                                1 (bases 1 to 65916)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP11-462C21
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Homo sapiens chromosome 17 clone RP11-462C21 map 17, LOW-PASS
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32560. 32701
                            /rpt_family="THE1B-internal"
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27209. 27509
...7pt_family="Alusx"
27564. 27747
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26883. .26991
                                                                                                                                                                /rpt_family="Alu"
25642. .25914
/rpt_family="Alux"
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33872. .34126
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33693. .33766
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AC083783.2 GI:13194285
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17 28516: gap of 100 bp 11 100 pp 13 2932: contig of 716 bp in length 29 33 2932: contig of 716 bp in length 33 30053: contig of 721 bp in length 100 bp 100
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16247 16948: contig of 702 bp in length
16949 17048: gap of 100 bp
17049 17741: contig of 693 bp in length
                                                                                                                                                                                                                                                                       10546: gap of 100 bp 11290: contig of 744 bp in length 11390: gap of 100 bp 12102: contig of 712 bp in length 12202: gap of 100 bp 122918: contig of 716 bp in length 122918: contig of 716 bp in length
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18671: gap of 100 bp
19416: contig of 745 bp in length
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23499: contig of 715 bp in length
24310: gap of 100 bp
100: gap of 100 bp
10: gap of 100 bp
25100: contig of 690 bp in length
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                                                                                                                                                                                      9704: gap of 100 bp
10446: contig of 742 bp in length
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37360: contig of 713 bp
60: gap of 100 bp
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36547: contig of 749 bp
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                                               8799: contig of 717
8899: gap of 100 br
9604: contig of 705
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 140368)
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4224: contig of 707 bp in length
42324: gap of 100 bp
43027: contig of 703 bp in length
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47966: contig of 707 bp in length
106: gap of 100 bp
48788: contig of 722 bp in length
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3.4e-27;
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41417: contig of 725 bp
41517: gap of 100 bp
42224: contig of 707 bp
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                                                39056: gap of 1.
39777: contig of
38274: gap of 1 1 38956: contig of
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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40592: cont
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LOCUS
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COMMENT

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Direct Submission
Submitted (23-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                      0.3%; Score 71; DB 74; Length 140368; 100.0%; Pred. No. 3.7e-27; Live 0; Mismatches 0; Indels 0;
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Center code: WUGSC
             gap of unknown length
contig of 5158 bp in length
gap of unknown length
gap of unknown length
contig of 5238 bp in length
contig of 5964 bp in length
gap of unknown length
contig of 6361 bp in length
gap of unknown length
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gap of unknown length
contig of 12197 bp in length
gap of unknown length
contig of 13600 bp in length
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Center project mame: H-W10174L18
Center project name: H-W10174L18
Sequencing vector: M13; 100%
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                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates;
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AC064852.1 GI:7637789
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                       Direct Submission
Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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                                                                                                                 MO 63108, USA
On Aug 12, 2000 this sequence version replaced gi:8571792.
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Center code: WUGSC
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Waterston, R.H.
The sequence of Homo sapiens clone Unpublished
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Waterston, R.H.
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2747: gap of unkn
4114: contig of 1
4214: gap of unkn
5700: contig of 1
5700: gap of unkn
7138: gap of unkn
7138: gap of unkn
8655: contig of 1
8655: gap of unkn
10525: gap of unkn
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          Chemistry: Dye-primer ET; 100% of reads
Assembly Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0,990319
Consensus quality: 144261 bases at least Q40
Consensus quality: 144261 bases at least Q30
Consensus quality: 148832 bases at least Q20
Insert size: 167000; agarose-fp
Insert size: 151830; sum-of-contigs
Quality coverage: 4.17 in Q20 bases; sum-of-contigs
Quality coverage: 4.65 in Q20 bases; sum-of-contigs
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/note="assembly_name:Contig6"
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/note="assembly_name:Contig7"
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/note="assembly_name:Contig4"
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/note="assembly_name:Contig5"
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/note="assembly_name:Contig3"
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Sequencing vector: plasmid; 0%
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/chromosome="2"
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Direct Submission
Submitted (08-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MMO 63108, USA
On Apr 27, 2000 this sequence version replaced gi:7107587.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 188679)
Waterston, R.H.
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/note="assembly_name:Contig19"
46549 a 32500 c 30533 g 42240 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC023121
AC023121.3 GI:7656637
HTG; HTGS_PHASE1; HTGS_DRAFT.
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Waterston, R.H.
                                                                clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.3%
Best Local Similarity 100.0
Matches 71; Conservative
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Gaps

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Indels

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Mismatches

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Conservative

71;

Matches

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
Chemistry: Dye-terminator Big Dye; 20% of reads Assembly program: Phrap; version 0.990319 consensus quality: 186330 bases at least Q40 Consensus quality: 186828 bases at least Q30 Consensus quality: 187104 bases at least Q20 Insert size: 195000; agarose-fp Insert size: 197779; sum-of-contigs Quality coverage: 7.15 in Q20 bases; sum-of-contigs Quality coverage: 7.45 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 57232: gap of unknown length

1233 72793: contig of 15561 bp in length

1294 72893: gap of unknown length

1248 96247: contig of 23354 bp in length

1248 96347: gap of unknown length

1348 122530: contig of 26183 bp in length

1531 122630: gap of unknown length

1548 122630: contig of 66049 bp in length

1550 188679: contig of 66049 bp in length.
                                                                                                                                                                                                                                                                                                                                                                             s: contig of 3458 bp in length
s: gap of unknown length
c: contig of 5187 bp in length
s: gap of unknown length
c: contig of 11753 bp in length
s: gap of unknown length
s: contig of 9640 bp in length
s: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 14269 bp in length
gap of unknown length
contig of 12325 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown length
of 12325 bp in length
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122631 . 188679
101016="assembly_name:Contig33"
143483 c 42231 g 51048 t
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/note="assembly_name:Contig24"
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/note="assembly_name:Cont1g30"
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10439. .44707
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/note="assembly_name:Contig25
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/note="assembly_name:Contig29
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/organism="Homo sapiens"
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/clone="RP11-296K10"
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20698:
30338:
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ORIGIN
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Length 188679;

Ouery Match 0.3%; Score 71; DB 67; Best Local Similarity, 100.0%; Pred. No. 3.9e-27;

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represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc. even if efforts are made to eliminate these contaminating sequences. The following BAC sequence is oriented from the T7 to the SP6 end.

Upstream BAC (overlapping the T7 end): R-45p15 (AC-AL138976)

Downstream BAC (overlapping the SP6 end): C-2538G10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (07-DEC-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
On Dec 9, 2000 this sequence version replaced gi:8247492.
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Qy 17379 ctcttgttgcccaggctggagtgcaatggcgtgatctcagctcactgcaacctccgcctc 17438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT: This sequence is unfinished and does not necessarly
                                                                                                                                                                                                                                                                           HTG 08-DEC-2000 HOMO Sapiens Chromosome 14 clone R-736N17, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percentage of bases with a quality value >= 40 : 99 %.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap; version 2.0 Quality coverage: 10.24x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Genoscope / Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.genoscope.cns.fr/
Contact: SegRef@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                      AL161669.4 GI:116111164
HTG; HTGS_PHASE2; HTGS_DRAFT.
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1. .192064
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19129
54514
99471
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Direct Submission
                                                                                                                                                     Db 151657 CCGGGTTCAAG 151647
                                                                                                     Oy 17439 ccgggttcaag 17449
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- 59
- 69
- 79
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TITLE
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KEYWORDS
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20479
22936 :
23036
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JOURNAL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                    identified using the e-PCR software (G. Schuler)"
103114. .103373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.3%; Score 71; DB 84; Length 192064; 100.0%; Pred. No. 3.9e-27; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-9B11 Unpublished
                                       /clone="R-736N17"
/clone_lib="RPCI-11"
27321. .27545
/note="matching EMBL:G04572
                                                                                                                                                                                                                                            /note="matching EMBL:M92357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="matching EMBL: H60047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 17 clos
SEQUENCE, 33 unordered pieces.
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC087691.2 GI:12957885
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                              .130217
                                                                                                                                                                                                                                                                                   dbSTS:STS14628
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                                                                                                                                                                          dbSTS:STS22999
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                                                                                                                              RHdb: RH53929
                                                                                                                                                                                                                                                                                                                                                                             RHdb: RH67603
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AC087691/c
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TITLE
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AUTHORS
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Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Soy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trajilo, J., Vassiliev, H., Vial, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
Contact sequence_submissions@genome.wi.mit.edu
Contact project Information
Center project name: 112351
Center clone name: 9 B.11
Center plasmid: n/a; 100% of reads
Centeristry: pye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 183023 bases at least Q40
Consensus quality: 189063 bases at least Q20
Consensus quality: 189063 bases at least Q20
Consensus quality: 189063 bases at least Q20
Consensus quality: 189063 bases; sum-of-contigs
Quality coverage: 6.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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contig of 982 bp in length
ap of 100 bp in length
contig of 1352 bp in length
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13920 15542: contig of 1623 bp in length
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15643 17701: contig of 2059 bp in length
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contig of 2577 bp in length
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25203: contig of 2168 bp in length
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f 881 bp in length
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of 700 bp in length
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Web site: http://www-seq.wi.mit.edu
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13819: con+
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3112: con
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4: gap of
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107608 107707: gap of 100 bp 100 bp 119748: contig of 12041 bp in length 119749 119848: contig of 12041 bp in length 119749 119972 13077: gap of 100 bp 129972 130071: gap of 100 bp 129972 130071: gap of 100 bp 130072 147185: contig of 17114 bp in length 147186 147285: gap of 100 bp 147286 165313: contig of 19028 bp in length 165314 166413: gap of 100 bp 165314 165413: gap of 100 bp 165314 165413 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 165414 1654
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7425: contig of 32122 bp in length
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1. .551
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'note="assembly_fragment"
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'note="assembly_fragment"
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30479. .22935
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/note="assembly_fragment"
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/note="assembly_fragment"
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23036. .25203
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'note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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Baker, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C.,
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Harris, K., Hotton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L.,
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Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence.
ACO05291
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Submitted (17-JUL-1998) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 198582)
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100.0%; Pred. No. 3.9e-27;
Live 0; Mismatches 0; Indels 0;
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Best Local Similarity 100.(
Matches 71; Conservative
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TITLE
JOURNAL
REFERENCE
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SOURCE
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Ye, W. J., Zhao, J. and Zody, M.
Direct Submission
AL Submission
AL Submitted (07-Augenene, Version replaced gi:3399679.
All repeats were identified using RepeatMasker: Smit, A.F.A. &
Green, P. (1996-1997)
All repeats were identified using RepeatMasker: Smit, A.F.A. &
Coganism-"Homo sapiens"
All repeats were identifiers
II. 198582
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complement(7677. .7966)
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/rpt_family="MER5B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59. .160
/rpt_family="L1MC5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome="17"
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  (bases 1 to 198582)
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REFERENCE
AUTHORS
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JOURNAL
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.17592)

"FLAM_C"

"MIR"

"MLT1G"

74% of reads

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Assembly program: Phrap; version 0.99319
Consensus quality: 19554 bases at least 040
Consensus quality: 19554 bases at least 030
Consensus quality: 19766 bases at least 030
Consensus quality: 197678 bases at least 030
Consensus quality: 197657 bases at least 030
Insert size: 1202248; sum-of-contigs
Quality coverage: 11.1x in 020 bases; sum-of-contigs.

* NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1678: contig of 1678 bp in length 1778: gap of unknown length 4963: contig of 3085 bp in length 4963: gap of unknown length 9565: contig of 4602 bp in length 15106: gap of unknown length 15206: gap of unknown length 15206: gap of unknown length 15206: gap of unknown length 24874: gap of unknown length 32122: contig of 7148 bp in length 42229: contig of 10007 bp in length 5229: contig of 10007 bp in length 5229: contig of 10007 bp in length 5229: gap of unknown length 5229: contig of 10007 bp in length 5229: contig of 10007 bp in length 5229: contig of 10037 bp in length 63923: contig of unknown length 16329: contig of unknown length 16329: contig of unknown length 16329: contig of unknown length 16403: gap of unknown length 16403: 
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of 11637 bp in length
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133783: gap of unknown length
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gap of unknown length
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203748: contig of 39955 bp in length.
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of 11991 bp in
                                                             Sequencing Vector: M13mp18; X02513
Chemistry: Dye-primer; 26% of reads
Chemistry: Dye-terminator Big Dye; 7
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1779. .4863
/note="assembly_name:Contig35"
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/note="assembly_name:Contig37"
15207. .24874
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24975. .32122
/note="assembly_name:Contig39"
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/note="assembly_name:Contig36"
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/organism="Homo sapiens"
              Center clone name: RP11-9B11
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/clone="RP11-9B11"
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163694
163794
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Homo sapiens chromosome 17 clone RP11-9B11, WORKING DRAFT SEQUENCE,
16 unordered pieces.
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1 (bases 1 to 203748)
Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Manado, J., Konp, C., Kottler, S., Lan, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, Oeffer, P., Palm, C.J., Ramirez, D., Southwick, A.M., Webb, C., Wilhelmy, J., Yu, S. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chases I to 203748)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Federsplei,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J.,
Ramirez,D., Wilhelmy,J., Yu,S. and Davis,R.W.
Direct Submission
Submistated (22-MAY-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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Center: Stanford DNA Sequencing and Technology Development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71; DB 85; I
Pred. No. 3.9e-27;
0; Mismatches 0;
/rpt_family="MLT1J"
complement(22715. .22824)
/rpt_family="MIR"
complement/?"
                                                                                                          complement(22855. .23109)
/rpt_family="AluSp"
complement(23110. .23192)
/rpt_family="MIR"
24077. .24285
                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="Alusx"
omplement'ser'
                                                                                                                                                                                                                                                                                                                             complement(25044...25171)
/rpt_family="MLT1A1"
25172...25469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26194. .26267
/rpt_family="purine-rich"
                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="AluSq"
complement(25470. ..
                                                                                                                                                                                                                                                      /rpt_family="Aluy"
complement(24558. .
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ilarity 100.0%; Pr
Conservative 0;
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AC069250.14 GI:13605982
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Best Local Similarity
'. hos 71; Conserve
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AC069250/c
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DEFINITION
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VERSION
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JOURNAL
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Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dear, K., Cooke, P., Donelan, L., Doyle, M., Perreira, P., Fitzhugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Maldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W., J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Only 94205 base pairs from the middle of this clone are being submitted. The remainder overlaps either accession number AC006948 (WICGR project L564) or accession number AC005243 (WICGR project
                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-JUN-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 1999 this sequence version replaced 91:5091642. All repeats were identified using RepeatMasker: Smit, A.F.A. 6 Green, p. (1996-1997)
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/clone_lib="RPCI-11 human BAC library"
/map="17"
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complement(8269. 8580)
/rpt_family="AluSq"
complement(10135. 10187)
/rpt_family="MIR"
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/rpt_family""MIR"
complement(11215. 11566)
/rpt_family""THEIA"
complement(11567. 11746)
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complement(13420. 13729)
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complement(13979. 14209)
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1992. .2248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(7212. 7350)
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7969. 8003
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4748. 4790
6378. .6451
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6855. .6888
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6895. .7210
/rpt_family="Allch"
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Bairren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,
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17, clone hRPK.57_A_1, complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 3.9e-27;
tive 0; Mismatches 0; Indels 0;
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                                                                                                                                             42330. .52186
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52287. .63923
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Best Local Similarity
Matches 71; Conservat
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complement(31749. .31810)
/rpt_family="L2"
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            /rpt_family="MIR"
complement(14378. .14505)
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2215. 3240
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Direct Submission

Submitted (26-MAY-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk clone
requests: clonerequest@sanger.ac.uk
on Jun 4, 2000 this sequence version replaced gi:8218296.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em., EMBL: Sw., SWISSPROT: Tr., TREMBL: Wp., WORMPEP: Information on the WORWPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 mapping droup. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
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Human DNA sequence from clone RPI1-264C15 on chromosome 9q32-34.11,
complete sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 130526)
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                                                                                                                                                                                                             /rpt_family="MLT1J"
complement'(1'.
                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="MER21B"
                                                                                                                                                                                                                                                                   complement(41421. .41576)
/rpt_family="MIR"
complement(41796. .41841)
                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="MER21A"
complement(42040. .42
/rpt_family="AluSq"
complement(39934. .
                                                                                              /rpt_family="MER20"
                                                                                                                                                                                              /rpt_family="AluSx"
                                                                                                                    complement(40347
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Db 89758 CCTTGTGATC 89749
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RP11-264C15 is from the library RPCI-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pBACG-3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-264C15 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-264C15 is at 1 in this sequence. The true left end of clone RP11-67K19 is at 130427 in this sequence. The true right end of clone RP11-67K19 is at 130427 in this
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACO26144 147990 bp DNA HTG 05-APR-2000 Homo sapiens chromosome 4 clone RP11-106H1 map 4, WORKING DRAFT SEQUENCE, 17 unordered pieces.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 4, clone RP11-106H1
Unpublished
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100.0%; Pred. No. 1.3e-26;
7ative 0; Mismatches 0;
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27088 c 27582 g 36865 t
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens'
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/clone="RP11-264C15"
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (19-MPK-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 5, 2000 this sequence version replaced g1:7264214.
                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 153000; agarose fp
Insert size: 146390; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
Quality coverage: 4.4 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                   Sequencing vectors M13, M77815; 100% of reads Sequencing vectors M13, M77815; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 137712 bases at least Q40 Consensus quality: 142871 bases at least Q30 consensus quality: 144908 bases at least Q20
                                                                                                                                                                                                            Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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£ 12533 bp in length
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65398: contig of 10846 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 1059: contig of 1059 bp in length
1060 1159: gap of 100 bp
1160 2331: contig of 1172 bp in length
2332 2431: gap of 100 bp
2432 4117: contig of 1686 bp in length
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of 4783 bp in length
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45548: contig of 8444 bp in length
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54452: contig of 8804 bp in length
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/db_xref="taxon:9606"
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Center clone name: 106_H_1
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represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc. . even if efforts are made to eliminate these contaminating sequences. The following BAC sequence is oriented from the 77 to the SP6 end): R-903H12

Downstream BAC (overlapping the 77 end): R-903H12

Downstream BAC (overlapping the SP6 end): R-84C10 (AC-AL355922)

Assembly program: Phrap; version 2.0

Quality coverage: 8.64x in Q20 bases; sum-of-contigs
             Submitted (30-JAN-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
On Dec 9, 2000 this sequence version replaced gi:6634066.
                                                                                                                                                                                                     IMPORTANT: This sequence is unfinished and does not necessarly
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Identified using the e-PCR software (G. Schuler)"
34326. .34475
Anotea-mail BBL:G15182
RHdb:RH14231
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Identified using the e-PCR software (G. Schuler)"
144244. .144399
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Identified using the e-PCR software (G. Schuler)"
53428. .53648
/note="matching EMBL:G14582
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
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                                                                                                         Center: Genoscope / Centre National de Sequencage
Center code: GS
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                                                                                                                                              Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
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RHdb:RH70907
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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66. .342
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Range: bases
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4390
15474
48563
92132
 Direct Submission
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However, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 162472)
Genoscope.
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14 clone R-219E7, *** SEQUENCING IN
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                                               /clone_lib="RPCI-11 Human Male BAC" 1. .1059
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hes 0;
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//note="assembly_fragment"
128098. ...147990
//note="assembly_fragment"
28973 c. 29088 g 43938 t
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/note="assembly_fragment"
4218. 6670
/note="assembly_fragment"
6771. 9681
/note="assembly_fragment
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/note="assembly_fragment"
14665. .22015
/note="assembly_fragment"
                                                                                      /note="assembly_fragment"
1160. .2331
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment
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PROGRESS ***, in ordered pieces
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                                 /clone="RP11-106H1"
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                                                                                                                                                                                                                                                                         vector_side:right"
/chromosome="4"
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I (Dassa 1 to 165464)

I (Dassa 1 to 165464)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Blangaqe, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., David, M.L., Davis, C., David, C., Claveland, C.D., Cox, C., Denn, A.L., Din, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dougan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Escotto, M., Falls, T., Ferraquto, D., Flago, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Garcia, A., Garner, T., Garza, N., Glill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hane, S., Hernandez, J., Hernandez, O., Hadris, K., Hart, M., Havlak, P., Hume, J., Joudah, S., Kalason, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Hume, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsedgh, H., Loulsegd, H., Louzado, M., Manna, T., Martin, D., Martin, D
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Homo sapiens chromosome 3 clone RP11-34L7, WORKING DRAFT SEQUENCE,
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Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
                                                                                                                                                                                                                                                                                                  dbsrs:srs28835
Identified using the e-PCR software (G. Schuler)"
154968 155213
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                                                                                               Identified using the e-PCR software (G. Schuler)" 154904...155170
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0.3%; Score 70; DB 83; Length 162472;
Best Local Similarity 100.0%; Pred. No. 1.4e-26;
Matches 70; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="matching EMBL: Z16878
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'note="matching EMBL:G11174
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                  dbSTS:STS25650
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RHdb:RH42199
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RHdb: RH12971
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Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N., Nauyen,M., Moyen,N., Nguyen,N., Nguyen,N., Nguyen,B., Novedon,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A. Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sison,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usman,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warlen,R., Washington,S., Wallalems,G., Walliamson,A., Walczyk,R., Wooden,S., Wallighton,S., Walliamson,A., Walczyk,R., Wooden,S., Wallighton,S., Walliamson,A., Walczyk,R., Wooden,S., Walczyk,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hdsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project name: RP11-34L7
Center clone name: RP11-34L7
Center clone name: RP11-34L7
Center clone name: RP11-34L7
Sequencing vector: M12 LOB821
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 153622 bases at least Q40
Consensus quality: 153622 bases at least Q30
Consensus quality: 159659 bases at least Q30
Consensus quality: 159659 bases at least Q30
Consensus quality: 15033; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 4.8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 15 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Or (bases 1 to 165464)

Worley, K.C.

Direct Submission

Of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Gon Jan 5, 2001 this sequence version replaced g1:8699653.

Center: Baylor College of Medicine
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Direct Submission
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157672:

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 12 contigs. The tirue order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as Thus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Watlington, S., Walliams, G., Williamson, A., Walezyk, R., Wooden, S., and Gibbs, K., Wu, C., Wu, Y., Wu, Y., Rushington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., and Gibbs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: Manage Mana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-NOV-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 70967 bp in length gap of unknown length contig of 9647 bp in length gap of unknown length gap of unknown length contig of 6006 bp in length gap of unknown length gap of unknown length gap of unknown length
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gap of unknown length
contig of 5132 bp in length
gap of unknown length
contig of 2490 bp in length
gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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8 169533: contig of 1446
Location/Qualifiers
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Direct Submission
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S Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alibooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bantsooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Banks, T., Banks, T., Banks, J., Boutch, J., Blumage, K., Blankenburg, K., Bonnin, D., Bouck, J., Boutch, J., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, T., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davida, C., Edgar, M., Polagac, O., Denn, A.L., Dunn, H.H., Douthwaite, K.J., Draper, H., Dunn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan, Rocha, S., Durbin, K.J., Ferraquto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gantz, P., Hawes, A., Hamilton, K., Harris, C., Hart, M., Havlak, P., Haues, S., Hamilton, K., Harris, C., Hart, M., Havlak, P., Hume, J., Jackson, E., Jacobson, B., Jia, M., Hollins, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L. Li, J., Li, J., Li, J., Li, J., Li, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, M., Martin, R., Martingar, R., Martindale, R., Lind, R., Martin, R., Martin, R., Martindale, R., Luna, R., Lucier, R., Luna, R., Martindale, R., Luna, R., Lucier, R., Luna, R., Luna, R., Martindale, R., Luna, R., Luna, R., Martindale, R., Luna, R., Luna, R., Lucier, R., Luna, R., Martin, R., Martin, R., Martindale, R., Luna, R., Martin, R., Liu, J., Liu, J., Liu, J., Liu, M., Liu, R., Liu, M., Liu, M.
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Homo sapiens chromosome 12 clone RP11-60E8, WORKING DRAFT SEQUENCE,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_FULLTOP.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Bakren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Bakren, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Carny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Depare, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Molla, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wuyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC007940 171841 bp DNA HTG 25-MAY-2000
Homo sapiens clone RP11-44C14, WORKING DRAFT SEQUENCE, 11 unordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-JUL-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced gi:7321478.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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------- Summary Statistics
Sequencing vector: M13; M77815; 88% of reads
Sequencing vector: Plasmid; n/a; %-0.1%% of reads
11.8734793187348Chemistry: Dye-primer-amersham; 88% of reads
                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                Gaps
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Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
                                                                                                                          1112 others
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 171841)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Unpublished
                                                                                                                                                                                                                        Ouery Match
0.3%; Score 70; DB 63; 1
Best Local Similarity 100.0%; Pred. No. 1.4e-26;
Matches 70; Conservative 0; Mismatches 0;
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                                                                                             /clone="RP11-60E8"
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AC007940.3 GI:8072418
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.169533
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source
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ORIGIN
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AUTHORS
TITLE
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VERSION
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REFERENCE
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JOURNAL
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SOURCE
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NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye; 12% of rea Assembly program: Phrap; version 0,960731 consensus quality: 163415 bases at least 040 consensus quality: 167585 bases at least 040 consensus quality: 167585 bases at least 030 consensus quality: 169143 bases at least 020 lineart size: 170000; agarose-fp insert size: 170841; sum-of-contigs
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contig of 1881 bp in length
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120490 120589: gap of 100 bp
120590 171841: contig of 51252 bp
Location/Qualifiers
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8008
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179743)
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Direct Submission
Submitted (19-7AN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 12, 2000 this sequence version replaced gi:9212944.
                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                SEQUENCING IN PROGRESS ***, 19 unordered pieces. AL162400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                       0.3%; Score 70; DB 60; Length 171841; ilarity 100.0%; Pred. No. 1.4e-26; Conservative 0; Mismatches 0; Indels 0;
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46763 46862: gap of 100 bp

46863 50027: contig of 3165 bp in length

50028 55974: contig of 5847 bp in length

55975 56074: gap of 100 bp

55975 56074: gap of 100 bp

56075 64453: contig of 8379 bp in length
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44612 44711: gap of 100 bp
44712 46762: contig of 2051 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64553: gap of 100 bp 74354: contig of 9801 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                    AL162400.5 GI:9796916
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                  Qy 10403 ctgcaacctc 10412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                       Query Match
Best Local Similarity
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64554
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AL162400/c
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human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACO74011 180462 bp DNA HTG 22-MAR-2001
Homo sapiens chromosome UNK clone RP11-780J6, WORKING DRAFT
SEQUENCE, 1 unordered pieces.
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                                                                                                                                                                                                                                                                                               Length 179743;
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Sequencing vector: plasmid; 7%
Chemistry: Dye-primer ET; 93% of reads
Chemistry: Dye-terminator Big Dye; 7% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 180365 bases at least Q40
Consensus quality: 180467 bases at least Q20
Insert size: 183000; agarose-fp
Insert size: 181641; sum-of-contigs
Quality coverage: 7.42 in Q20 bases; sum-of-contigs
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN
             /note="assembly_fragment:01775"
171028. 173259_fragment:01975"
/note="assembly_fragment:01999"
/note="assembly_fragment:02016
fragment_chain:3"
17534. 179743
/note="assembly_fragment:01457
fragment_chain:3"
clone_end:r7
                                                                                                                                                                                                                                                                                             Query Match

0.3%; Score 70; DB 79; I
Best Local Similarity 100.0%; Pred. No. 1.4e-26;
Matches 70; Conservative 0; Mismatches 0;
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53015 a 36183 c 36336 g 52405 t
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.170927
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Waterston, R.H.
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Waterston, R.H.
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 19315)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Bonnin, D., Bouck, J., Bunage, K., Bonnin, D., Bouck, J., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Chen, G., Chen, R., Chen, R., Chendy, J., Charstopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davin, H.L., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hatt, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, J., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Lewis, L.E., Jacobson, B., Jia, Y., Johnson, R., Jau, Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Ludy, L., Li, Z., Lichtarge, O., Lieu, C., Ludy, Luna, R., Luds, Martinez, E., Massey, E., Mawhiney, E., Martinez, P., Martinez, E., Massey, E., Maueliney, E., Morecol, M.P., Meador, M., Martinez, E., Massey, E., Maueliney, E., Merchandez, Martinez, E., Massey, E., Maueliney, E., Merchandez, M., Martinez, E., Massey, E., Merchandez, Martinez, E., Massey, E., Merchandez, Martinez, E., Massey, E., Merchandez, Martinez, E., Massey, E., Martinez, E., Massey, E., Merchandez, Martinez, E., Massey, E., Martinez, E., Massey, E., Merchandez, Martinez, E., Massey, E., Martinez, E., M
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* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Best Local Similarity 100.0%; Pred. No. 1.4e-26;
Matches 70; Conservative 0; Mismatches 0;
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48849 a 42940 c 42516 g 46157
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1. .180462
/organism="Homo sapiens"
/db_xref="taxon:9606"
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BASE COUNT
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Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkovo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Patch,B., Perey,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Sibes,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tang,H., Tansey,J., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usman,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Thomas,M., Watlington,S., Wall,R., Wall,R.
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Center Clone name: RP11-53315

Sequencing vector: plasmid M7789
Sequencing vector: plasmid M7789
Sequencing vector: M13 L08817
Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-primer Diglety Dye: 98% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 187995 bases at least Q40
Consensus quality: 187995 bases at least Q30
Consensus quality: 189362 bases at least Q30
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On Jan 12, 2001 His sequence version replaced gi:11596949,
Center: Baylor College of Medicine
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contig of 36959 bp in length
gap of unknown length
gap of unknown length
contig of 34359 bp in length
contig of 34359 bp in length
contig of 26400 bp in length
gap of unknown length
contig of 8767 bp in length
gap of unknown length
contig of 6564 bp in length
contig of 7155 bp in length
gap of unknown length
gap of unknown length
contig of 7155 bp in length
gap of unknown length
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contig of 1804 bp in length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Unpublished
2 (bases 1 to 193159)
Worley, K.C.
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61057:
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1 (bases 1 to 194405)
Bliren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 4, clone RP11-600D20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (03-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 0214, USA On Jun 25, 2000 this sequence version replaced gi:7387412. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                 AC032004 194405 bp DNA HTG 25-JUN-2000 Homo sapiens chromosome 4 clone RP11-600D20 map 4, WORKING DRAFT SEQUENCE, 27 unordered pieces.
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190715: gap of unknown length
192029: contig of 1314 bp in length
192129: gap of unknown length
193159: contig of 1030 bp in length.
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131289 131388: gap of 100 bp 131389 148135: contig of 16747 bp in length 148136 148235: gap of 100 bp 148236 172729 172839: gap of 100 bp 172829 194405: contig of 21577 bp in length. Location/Qualifiers
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                                                                                                                               FEATURES
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                 Center project name: 18253

Center clone name: 600_D_20

Center clone name: 600_D_20

Sequencing vector: M13: M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 179734 bases at least Q40
Consensus quality: 187831 bases at least Q30
Consensus quality: 190379 bases at least Q20
Insert size: 192000; agarose-fp
Insert size: 191805; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; sum-of-contigs
                                Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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1388 1487: gap of 100 bp
1488 2669: contig of 1182 bp in length
2570 2769: gap of 100 bp
2770 4072: contig of 1303 bp in length
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23667: contig of 2678 bp in length
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26382: contig of 2615 bp in length
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31356: contig of 4874 bp in length
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43693: contig of 7733 bp in length
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Muzny, D.M., Adams, C., Addo-Oduola, B., All-osman, F.R., Allen, C., Alsbrooks, S. L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Burcoks, S. L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Burcoks, S. L., Amaratunge, H.C., Are, J.R., Brown, M., Bryant, N.P., Burch, J., Burch, P., Burch, P., Burch, P., Burch, P., Carron, T.E., Carren, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Carren, R., Carter, M., Cavazos, S.R., David, R., David, M.D., Davis, C.C., Coyle, M.D., David, R., David, R., Davis, C.D., Cox, C., Coyle, M.D., Davis, C.D., Dinh, H.H., Douthwaite, R.J., Draper, H., Davy-Carroll, L., Dederitch, D.A., Delaney, R.R., Davis, C.C., Edgar, D., Edgar, D., Edgar, D., Edgar, D., Edgar, D., Edgar, D., Ford, J., Foster, P., Frantz, C., Harris, K. Harris, K. Harris, C., Harris, K., Harris, C., Harris, C., Harris, K., Harris, K., Harris, C., Harris, C., Harris, K., Harris, K., Harlak, P., Hawes, A., Hamllton, K., Harris, C., Harris, K., Harris, K., Hally, S., Hume, J., Jackson, L.E., Jacobson, B., Jal, Y., Obnson, R., Johnson, R., Johnson, R., Johnson, R., Marison, E., Massey, E., Modgon, A., Houses, M., Holloway, C., Liu, J., Liu, J., Liu, R., Lucier, R., Lucier, R., Lund, R., Martindale, A., Martindale, A., Martindale, A., Massey, E., Maxhiney, E., McLeod, M.P., Mayle, R., Maxhiney, E., McLeod, M.P., Mayle, M., Mayusen, N., Mayusen, N., Midoyen, N., Mayusen, N., Maked, S., Savery, C., Savery, C., Sparks, A., Spachey, T., Succept, R., Thomas, N., Tamerisa, K., Tamay, H., Tanay, H., Wallians, G., Williams, G., Wallians, G., Wa
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                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 305583)
                                                                                                                                                                                                  Qy 10343 ttttgagacagagtctcgctctgtcaccaggctggagtgcagtggtgcgatcttggctca 10402
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                                                                                                  Length 194405;
     2606 others
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                                                                                                                           1.4e-26;
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100.0%; Pred. No. 1.4e-26
56398 a 39349 c 40959 g 55093 t
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+'ve 0; Mismatches
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Chemistry: Dye-primar Bodipy: 32% of reads
Chemistry: Dye-primator Big Dye: 68% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 249729 bases at least Q40
Consensus quality: 283537 bases at least Q30
Consensus quality: 297805 bases at least Q30
Consensus quality: 27805 bases at least Q30
Consensus quality: 27805 bases at least Q30
Consensus quality: 297805 bases at least Q30
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Consensus quality: 297805 bases at least Q30
Quality coverage: 2.9x in Q20 bases; sum-of-contigs estimation
Quality coverage: 2.9x in Q20 bases; sum-of-contigs estimation
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NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 95 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Submitted (24-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Mar 1, 2001 this sequence version replaced gi:13162454.
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                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                              Center: Baylor College of Medicine
Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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Matches 70; Conservative 0; Mismatches
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Center clone name: 798_G_7
                                                                                                                                                                                              Homo sapiens chromosome
SEQUENCE SAMPLING.
                                                                                                                                                                                                                                 AC091132.1 GI:13493096
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                                                                                                                                                                                   60280 bp
                                                                                                                                                                                                                                                HTG; HTGS_PHASE0
                                                                                                             111111111
70637 CCGGGTTCAA 70646
                                                                                               Oy 17439 ccgggttcaa 17448
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  Query Match
                                                                                                                                                                                             DEFINITION
                                                                                                                                                            83
                                                                                                                                                                                                                                                                        ORGANISM
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AUTHORS
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JOURNAL
REFERENCE
AUTHORS
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KEYWORDS
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                                                                                                                                                            RESULT
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overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                    75 11374; gap of 100 bp 12087; contig of 713 bp in length 180 12913; contig of 726 bp in length 19013; gap of 100 bp 100 bp 13737; contig of 726 bp in length 13013; gap of 100 bp 100 bp 180 13837; gap of 100 bp 100 bp 180 14544; contig of 707 bp in length 180 14544; contig of 707 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp
f 714 bp in length
100 bp
f 723 bp in length
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[ 714 bp in length
100 bp
[ 704 bp in length
                                                             705: contig of 705 bp in length
805: gap of
1100 bp
1510: contig of 705 bp in length
100: gap of
2326: contig of 716 bp in length
2426: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26152: gap of 100 bp
26869: contig of 717 bp in length
26969: gap of 100 bp
27670: contig of 701 bp in length
27770: gap of 100 bp
                                                                                                                                                                                                                                                    f 712 bp in length
100 bp
f 701 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69: gap of 100 bp 16198: contig of 729 bp in length
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709 bp in length
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708 bp in length
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696 bp in length
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25231: contig of 727 bp
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23576: contig of
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19513: contig of
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18699: contig of
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58: gap of 1
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5583: c
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6386: c
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10465: c
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7198:
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in length in length length 100 bp 730 bp in length in length in length length length in length in length in length in length in length in length : 701 bp in length 100 bp in ţu in in in in įυ ţu in in ţ 731 bp in 100 bp 2655: gap of 100 bp 33369: contig of 714 bp in 3469: gap of 100 bp 34167: contig of 698 bp in 1267: gap of 100 bp 13479: contig of 712 bp in 1079: gap of 100 bp in 135786: contig of 707 bp in 100 2209: gap of 100 bp 30920: contig of 711 bp 11 lp 11 lp 12 l 7287: gap of 100 bp 47998: contig of 711 bp in 100 bp 100 100 bp 732 bp 3 100 bp 100 bp 701 bp 100 bp 722 bp 100 bp 723 bp 100 bp 723 bp 45643: gap of 100 bp 46372: contig of 729 bp 46472: gap of 100 bp 47187: contig of 715 bp 100 bp 719 bp 100 bp 730 bp 44823: gap of 100 bp 45543: contig of 720 bp 45643: gap of 100 bp 66: gap of 100 bp 29282: contig of 716 bp 82: gap of 100 bp 30109: contig of 727 bp 44007: gap of 100 bp 44723: contig of 716 bp 522: gap of 100 bp 52078: contig of 726 bp 715 bp dq 001 48098: gap of 48799: contig of 7 48899: gap of 49618: contig of 7 31020: gap of 10 31734: contig of gap of 1 86: gap of 1 36587: contig of 36687: gap of 1 37417: contig of 139: gap of 1 42261: contig of 61: gap of 1 43084: contig of 33: gap of 1 51252: contig of 53819: gap of 1 54551: contig of 55482: gap of 1 56183: contig of 56283: gap of 1 contig of 50433: contig of contig of contig of 53719: contig of 55382: contig of 184: gap of 43907: cont. gap of gap of gap of gap of 52889 33469: 51352: 31834: 32655: 41539: 43184: 47287: 49718: 29382: 52178: 35886: 35079: 28566 34267 52989 42361 50533 54651 35080 35787 37418 37518 55383 55483 56184 19619 51253 51353

Score 69; DB 78; Length 60280; Pred. No. 4.4e-26;

0.3%; S 100.0%;

Query Match Best Local Similarity

LOCUS

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boqualavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Moccones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollaraw, V., Rilegy, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC011979 137641 bp DNA HTG 30-MAR-2000
Homo sapiens clone RP11-16F15, WORKING DRAFT SEQUENCE, 30 unordered
homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 137641)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-16F15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Transcription factor (TFIIIC) alpha chain, partial)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 114411;
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4.8e-26;
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101138. .101255
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AC011979.3 GI:7341927
HTG; HTGS_PHASE1; HTGS_DRAFT.
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On Jan 25, 1998 this sequence version replaced gi:2642422.
Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA e-mail address: mdadams@tigr.org. The Orientation of the sequence is from SP6 end to 77 end. Genes were identified by a combination of five methods including: XGRALL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.Edu/chris/GENSCANW.html)searches of the complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hgi/html). Genes without pepetide
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                                                                                                                                                                                                                                                                                                                          HUACO02551 114411 bp DNA PRI 23-NOV-1999
Human Chromosome 16 BAC clone CIT987SK-A-951C11, complete sequence.
ACO02551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryofta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 11441)

Loftus, B.J., Kim, U.J., Sneddon, V.P., Kalush, F., Brandon, R., Fuhrmann, J., Mason, T., Crosby, M.L., Barnstead, M., Cronin, L., Deslattes Mays, A., Cao, Y., Xu, R.X., Kang, H.L., Mitchell, S., Eichler, E., Harris, P.C., Venter, J.C. and Adams, M.D. Genome duplications and other features in 12 Mb of DNA sequence (From human chromosome 16p and 16q Genomics 60 (3), 295-308 (1999)
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Direct Submission
Submitted (05-FEB-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
7 (bases 1 to 114411)
Adams, M.D. and Loftus, B.J.
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Submitted (19-SEP-1997) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
4 (bases 1 to 114411)
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Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J.,
Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C.
Human Chromosome 16 BAC clone CIT987SK-A-951C11
          Indels
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          Conservative
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HUAC002551
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Gaps

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Indels

TITLE JOURNAL COMMENT

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113381 113480: gap of 100 bp

113481 122965: contig of 9485 bp in length

122966 123065: gap of 100 bp

123066 137641: contig of 14576 bp in length.

Location/Qualifiers
                                                                                                                                              64602: gap of 100 bp 72223: contig of 7621 bp in length
                                                                                                                                                                                                                                                                    88138 88237: gap of 100 bp
88238 96553: contig of 8316 bp in length
96554 96553: gap of 100 bp
96654 105243: contig of 8590 bp in length
                         48802: gap of 100 bp
53681: contig of 4879 bp in length
                                                             81: gap of 100 bp 58325: contig of 4544 bp in length
                                                                                                                                                                                      23: gap of 100 bp
79639: contig of 7316 bp in length
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105344 113380: contig of 8037 bp in length
      48702: contig of 5437 bp in length
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1. .1611
                                                                                                     58425: gap of 100 bp 64502: contig of 6077 bp
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10914. .12550
/note="assembly_fragment"
12751. .14999
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/note="assembly_fragment"
26362. 29293
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29394. 33323
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19576. .22387
/note="assembly_fragment"
22488. .23255
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'note="assembly_fragment"
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note="assembly_fragment"
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5100, .17144
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/note="assembly_fragment"
43266. .48702
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/note="assembly_fragment"
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7245. .19475
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13424. .38990
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/note="assembly_fragment"
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/note="assembly_fragment"
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/db_xref="taxon:9606"
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53782 58325:
58782 6450: gail
64503 64602: gail
64603 72223:
7224 7323: gail
73640 79739: gail
7940 88137: gail
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Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-oCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 30, 2000 this sequence version replaced gi:6453971.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 3.4 in Q20 bases; agarose-fp Quality coverage: 3.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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1612 1711: gap of 100 bp
1712 3086: contig of 1375 bp in length
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contig of 1404 bp in length
of 100 bp
contig of 1242 bp in length
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f 1526 bp in length
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19475: contig of 2231 bp in length
19575: gap of 100 bp
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29293: contig of 2932 bp in length
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10813: contig of 1639 bp in length
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14999: contig of 2249 bp in length
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Insert size: 134741; sum-of-contigs
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3087 3186: gap o
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26362 29293
29294 29393:
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17145 17244:
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19476 19575:
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Estimated insert size: 153120; sum-of-contigs estimation Quality coverage: 3.94 in Q20 bases; pulse field gel estimation Quality coverage: 3.78 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a "working draft' sequence. It currently consists of 12 contigs. Gaps between the contigs are represented as runs of N. The order of the pleces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have submittor:

* This sequence will be replaced by the submittor:

* This sequence will be replaced the sequence as soon as it is available and the accession number will be preserved.

* By the finished sequence as soon as it is available and size a submittor:

* This sequence will be replaced to the finished sequence as soon as it is available and size a submittor:

* This sequence will be preserved.

* This sequence will be preserved.

* This sequence will be preserved.

* By the finished sequence as soon as it is available and size a submittor.

* This sequence will be preserved.

* By the finished sequence as soon as it is available and size a submitter to the property.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 154577)
Burton,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens chromosome 6 clone RP11-689K9, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces.
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HTG; HTGS_PHASE1.
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Catarrhini; Hominidae; Homo.
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Consensus quality: 150906 bases at least 030
Consensus quality: 151921 bases at least 020
Estimated insert size: 147000; pulse field gel estimation
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Best Local Similarity 100.0%; Pred. No. 4.9e-26;
Matches 69; Conservative 0; Mismatches 0;
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123066. 137641
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1 29416 c 27916 g 38239 t
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79740. 88137
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96654. 1105243
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105344. 113380
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113481. 1122965
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 153620)
DOE Joint Genome Institute.
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AC026709.4 GI:9954678
HTG; HTGS_PHASE2; HTGS_DRAFT.
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137659 144322: contig of 6664 bp in length 144323 144422: gap of 100 bp 144423 14769: contig of 3047 bp in length 147470 14759: gap of 100 bp 100 bp 147570 154577: contig of 7008 bp in length. Location/Qualifiers
  100 bp
6664 bp in length
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1. 20042
1. 20042
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1. 20043
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  137559 137658: gap of
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                                                                                                                                                                source
                                                                                                                                          FEATURES
Direct Submission
Submitted (21-2NA-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                            Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Bly Dye; 100% of reads
Consensus quality: 138465 bases at least Q40
Consensus quality: 144377 bases at least Q30
Consensus quality: 144377 bases at least Q30
Insert size: 152277; sum-of-contigs
Insert size: 183673; agarose-fp
Quality coverage: 3.10x in Q20 bases; sum-of-contigs Quality
coverage: 2.91x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                        103230 1001321 CUILLY 01 223.0 by in teny 0.1 106129 106292 gap of 100 bp 106293 1084531 contig of 2161 bp in length 108454 1021851 contig of 3632 bp in length 112186 112285 gap of 100 bp 100 bp 117286 1175481 gap of 100 bp 117649 1176481 gap of 100 bp 117649 1176481 gap of 100 bp 117649 1176441 gap of 100 bp 120244 1273741 contig of 7131 bp in length 120375 127441 gap of 100 bp
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91789: contig of 6708 bp in length
889: gap of 100 bp
96630: contig of 4741 bp in length
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127475 131033: contig of 3559 bp in length
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131134 134291: contig of 3158 bp in length
134292 134391: gap of 100 bp
134392 137558: contig of 3167 bp in length
                                                                                                                                                                                                      Contact: humquery@sanger.ac.uk
                                                                                                                                                                                   site: http://www.sanger.ac.uk
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                                                                                                                                                                                                                                                      Center project name: bA689K9
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                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 168111)
                                                                                                     Length 154577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                   2323 others
                                                                                                                                                                                                                                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 2, clone RP11-105K20 Unpublished
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144423 .147469
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147570 .154577
/note="assembly_fragment:01169"
28895 c 29003 g 46447 t 23
                                                                                                  0.3%; Score 69; DB 80;
100.0%; Pred. No. 5e-26;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: L6900
                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                            DNA.
                                                                                                                                                                                                                                                                                                                                  AC025788
AC025788.4 GI:10280878
                                                                                                                                                                                                                                                                                             168111 bp
                                                                                                  Query Match . 0.39
Best Local Similarity 100.
Matches 69; Conservative
                                                                                                                                                                                                                              Db 81426 recercade 81418
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TITLE
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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                  ACCESSION
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SOURCE
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                    Insert size: 173000; agarose-fp
Insert size: 165311; sum-of-contigs
Quality coverage: 3.4 in Q20 bases; agarose-fp
Quality coverage: 3.5 in Q20 bases; sum-of-contigs
                     Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 146760 bases at least Q40 consensus quality: 157693 bases at least Q20 consensus quality: 162037 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 bp
9 of 1365 bp in length
100 bp
9 of 1003 bp in length
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2982 bp in length
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8130 bp in length
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10120: contig of 1911 bp in length
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13572: contig of 3352 bp in length
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29242: contig of 3810 bp in length
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36856: contig of 4432 bp in length
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41393: contig of 4437 bp in length
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contig of 5844 bp in length
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contig of 5642 bp in length
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6057 bp in length
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contig of 3886 bp in length
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46862: contig of 5369 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5980 bp in length
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contig of 7832 bp
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.--- Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 526: gap of 100
527 1891: contig of
1892 1991: gap of 10
1992 2994: contig of
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64705: contig
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87124: contig
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clone_end:T7

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125129 137367: contig of 12239 bp in length 137368 137467: gap of 100 bp 137468 153264: contig of 15797 bp in length 153265 153344: gap of 100 bp 153365 168111: contig of 14747 bp in length.
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1. .168111
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527. .1891
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Stren, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Saldwin, J., Barna, N., Beda, F., Boguslavkiy, L.,
Anderson, S., Baldwin, J., Burkett, G., Campopiano, A., Castle, A.,
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Penestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D.,
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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
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Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,
McEwan, P., McGurk, A., McKernan, K., Morbheeters, R., Medlafin, J.,
Meneus, L., Mihova, T., Miranda, C., Pollara, V., Raymond, C.,
Riley, R., Pierre, N., Pisani, C., Pollara, V., Raymond, C.,
Subraman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M.,
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Subramanian, A., Talalmas, J., Tesfaye, S., Theodore, J., Tirrell, A.,
Travers, M., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B.,
Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and
Zody, M., Shando, S., Schoer, S., and Sainoun, J., Zimmer, A. and
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Homo sapiens chromosome 18 clone RP11-35B18 map 18, WORKING DRAFT
SEQUENCE, 19 unordered pieces.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-35B18
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                             Length 168111;
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1 Similarity 100.0%; Pred. No. 5.1e-26;
69; Conservative 0; Mismatches 0; Indels
                          2816 others
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49155 a 34309 c 33626 g 48205 t
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AC023388.2 GI:7139714
HTG; HTGS_PHASE1; HTGS_DRAFT.
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Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 157982 bases at least Q40 Consensus quality: 163050 bases at least Q20 Consensus quality: 165225 bases at least Q20 Insert size: 170000; agarose-fp Insert size: 167044; sum-of-contigs Quality coverage: 4.6 in Q20 bases; sum-of-contigs Quality coverage: 4.7 in Q20 bases; sum-of-contigs
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97996 115061: contig of 17066 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1743: contig of 1743 bp in length
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23451: contig of 4990 bp in length
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40238: contig of 5813 bp in length
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46534: contig of 6196 bp in length
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Submitted (14-JAN-2000) Genome Sequencing Center, Washington
Intersity School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 17, 2000 this sequence version replaced 91:7272322.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 171901)
Waterston, R.H.
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5 clone RP11-699022, WORKING DRAFT
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0.3%; Score 69; DB 68; Best Local Similarity 100.0%; Pred. No. 5.1e-26; Matches 69; Conservative 0; Mismatches 0;
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1 38724 c 38852 g 45489 t
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34426. .40238
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SEQUENCE, 24 unordered pieces
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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28787. .34325 ·
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Waterston, R.H.
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clone_end:T7
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                                 Center: Washington University Genome Sequencing Center
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unknown length
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of 13883 bp in length
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of 8965 bp in length
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Chemistry: Dye-primer ET; 838 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 156170 bases at least 040
Consensus quality: 161910 bases at least 030
Consensus quality: 164825 bases at least 030
Insert size: 179000; agarose-fp
Insert size: 169601; sum-of-contigs
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100.0%; Pred. No. 5.1e-26;
iive 0; Mismatches 0; Indels 0;
153469: gap of unknown length 171901: contig of 18432 bp in length.
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96614. .105578
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8010. 10174
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81204. .88841
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45428 a 38998 c 39575 g 45592 t
                                                                                                             /note="assembly_name:Contig10"
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/db_xref="taxon:9606"
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/clone="RP11-699022"
                    Location/Qualifiers
1. .171901
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153470. .171901
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150534 150633: gap of 100 bp
150634 177129: contig of 26496 bp in length.
Location/Qualifiers
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69023: contig of 10194 bp in length
123: gap of 100 bp
77125: contig of 8002 bp in length
                                                                                                                                                                         contig of 1961 bp in length of 100 bp contig of 1961 bp in length of 1568 bp in length
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                                                  contig of 1124 bp in length of 100 bp contig of 1247 bp in length
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25906: contig of 4466 bp in length
06: gap of 100 bp
36950: contig of 3944 bp in length
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41510: contig of 4460 bp in length
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                                                                                                                                  of 100 bp contig of 2032 bp in length
                                                                                                                                                                                                                                                                                              of 100 bp
contig of 3318 bp in length
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28260: contig of 3080 bp in length
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14880: contig of 3030 bp
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/db_xref="taxon:9606"
/chromosome="18"
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Signature.

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Baschien, V., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, N., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Klein, J., Lancoque, K., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lancoque, K., Jones, C., Kann, L., Karatas, N., McCarthy, M., McEwan, P., McGurk, J., McKernan, K., MoPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., MoPheeters, R., Meldrill, J., Meneus, L., Mihova, T., Miranda, C., Minoya, V., Morrow, J., Mirand, C., Pollara, V., Norman, C.H., O'Connor, T., O'Donnell, P., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Valler, Y., Voiel, R., Voia, R., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zahnoun, J., Zimmer, A., and Zody, M., Trayers, M., Zahnoun, J., Zimmer, A., and Zody, M., Subission, J., Zimmer, A., and J.
                                                                                              HTG 12-MAY-2000
Homo sapiens chromosome 18 clone RP11-586H24 map 18, WORKING DRAFT
SCOGNOC, 25 unordered pieces.
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                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Insert size: 17479; sum-of-contigs
Quality coverage: 3.6 in 020 bases; agarose-fp
Quality coverage: 3.6 in 020 bases; sum-of-contigs
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179947)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-44J9
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ilarity 100.0%; Pred. No. 5.1e-26;
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BASE COUNT ORIGIN

Matches

RESULT 93

AL355305

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL

COMMENT

AUTHORS REFERENCE

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hote-"Tandem repeat. Forced join. Gap size estimated to be approximately 750bp by restriction enzyme digest data." complement(11329. 11551)

Anote-"Sequence from overlapping clones bA787122 (EMBL accession AL390208) & bA689K9 (EMBL accession AL357046). Assembly confirmed by restriction digest."

Anote-"LiMa5A repeat: matches 5757. .6295 of consensus" complement(14960. 115375).
                                                                                                                                                                             Acte="match: GSS: Em:AQ714702"

2036. .2336

Anote="match: GSS: Em:AQ714702"

2036. .2336

Anote="180 copies 2 mer aa 56% conserved"

2787. .2924

Anote="Auv repeat: matches 1. .295 of consensus"

1787. .2924

Anote="Alux repeat: matches 1. .312 of consensus"

17837. .7857

Anote="Link repeat: matches 1. .312 of consensus"

17837. .2857

Anote="Link repeat: matches 2318. .4838 of consensus"

1817. .886

Anote="Link repeat: matches 1. .312 of consensus"

1817. .896

Anote="Link repeat: matches 1. .325 of consensus"

1817. .896

Anote="Link repeat: matches 1. .295 of consensus"

1860. .9318

Anote="Alux repeat: matches 1802. .2710 of consensus"

1861. .886

Anote="Alux repeat: matches 1802. .2710 of consensus"

1861. .886

Anote="Alux repeat: matches 1802. .2710 of consensus"

1861. .11362

Anote="Consensus"

1861. .11362

Anote="Consensus"

1862. .1073

Anote="Consensus"

1863. .11362

Anote="Consensus"

Anote="C
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15857. .15902
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17204. .17521
/note="L2 repeat: matches 2177. .2481 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SVA repeat: matches 1. .954 of consensus" 10879
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/note="16 copies 2 mer tg 93% conserved" 17022. .17176
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/note="match: GSS: Em:AQ387274"
19206, .19515
/clone_lib="RPCI-11.2"
6. .477
/note="match: GSS: Em:AQ702346"
                                                                                                                              Em: AQ727088"
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                                                                                                  7. .453
/note="match: GSS:
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On Oct 11, 2000 this sequence version replaced gi:10715951.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP, Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
RPRI-487F23 is from the library RPCI-11.2 constructed at the ROSWell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
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Human DNA sequence from clone RP11-487F23 on chromosome 6, complete
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Frankland,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is the entire insert of clone RP11-487F23 The true left end of clone RP3-491C16 is at 115276 in this sequence. The true right end of clone RP11-787122 is at 59873 in this sequence.
                                                                                                                                                                                                                                                                                                                                                     Gaps
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/note="assembly_fragment"
81176. .17947
/note="assembly_fragment"
a 31579 c 31342 g 57385 t
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100.0%; Pred. No. 5.16
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/clone="RP11-487F23"
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                                  misc_feature
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.2481 of consensus"

FEATURES

.2750 of consensus"

consensus

/note="Sequence from overlapping clones bA787122

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/note="Sequence from overlapping clones ba787122 (EMBL accession AL390208) & ba689K9 (EMBL accession AL357046). Assembly confirmed by restriction digest."
                                                                                                                                       21614. 21689 // Anote="Sequence from overlapping clone bA787122 (EMBL accession AL390208). Assembly confirmed by restriction
                                                                                                                                                                                                              21690. .21693
/note="Sequence from overlapping clone bA787122 (EMBL
accession AL390208). Assembly confirmed by restriction
                                                                                                                                                                                                                                                                  digest."
21923. 21922
27847A repeat: matches 1. .151 of consensus.
21923. .22124
7note="ALUJD repeat: matches 87. .287 of consensus."
7note="MER7A repeat: matches 151. .346 of consensus."
23355. .23439
7note="WGR7A repeat: matches 151. .346 of consensus."
23356. .23439
23889- .23966
                               20452. .20513
/note="MLT1J repeat: matches 112. .181 of consensus"
20569. .21116
                                                                                                                        'note="MLT1J repeat: matches 388. .516 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L2 repeat: matches 2236. .2487 of consensus"
20681. .26794
20681. ac794 repeat: matches 1. .333 of consensus"
27718. .27757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34485. .34595
/note="L2 repeat: matches 2134. .2245 of consensus"
34641. .34738
/note="MERSA repeat: matches 9. .105 of consensus"
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37792. .38105
                                                                       /note="MLTIF repeat: matches 1. .531 of consensus"
21225. .21341
                'note="AluJo repeat: matches 3. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MER7A repeat: matches 1. .346 of consensus" complement(38225. .38666)
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36864. .37003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anote="Mix repeat: matches 2. .144 of consensus" 37053. .37173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="39 copies 2 mer ca 70% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4920. .35146
fnote="L2 repeat: matches 2498.
85253. .35368
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clone RP11-948G15 map 17, WORKING DRAFT
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-948G15
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accession AL390208) & bA689K9 (EMBL accession AL357046) Assembly confirmed by restriction digest."
                                                                                                                                                                                                                                      8902 gigcagiggcacaatcicggcicactgcagcciccaccicccaggitcaagigaticicc 8961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                 Length 185257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                  core 69; DB 90; Length Low
Pred. No. 5.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: 948_G_15
------ Summary Statistics
Sequencing vector: M13; M77815; 40% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seg.wi.mit.edu
                                                                                                                   Similarity 100.0%; Pred. No. 5.1
                                                                                                        Score 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...... 189149 bp DNA
Homo sapiens chromosome 17 clor
SEQUENCE, 14 unordered pieces.
AC046171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC046171.3 GI:13184209
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
                                                                                                        0.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           8962 tgcctcage 8970
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                                                                                                     Query Match
Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
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JOURNAL
                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
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                                                                                                                                                                                                                                         δy
                                                                                                                                                                                                                                                                                                                                                                           δy
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Sequencing vector: Plasmid; n/a; 60% of reads

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ORIGIN
Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap: version 0.960731
Consensus quality: 185448 bases at least 040
Consensus quality: 18595 bases at least 040
Consensus quality: 187556 bases at least 020
Insert size: 196000; agarose-fp
Insert size: 197849; sum-of-contigs
Quality coverage: 10.0 in 020 bases; agarose-fp
Quality coverage: 10.1 in 020.
* NOTE: This is a "working" draft' sequence. It currently
consists of 14 contigs. The true order of the pieces
is not known and their order in this sequence record is
runs of N. but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106945 106944; contig or 106945 107044; gap of 100 bp 107044 129146; contig of 22102 bp in length 107045 129247 129246; gap of 100 bp 129247 157583; contig of 28337 bp in length 109247 157583; contig of 28337 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24712 24811: gap of 100 bp
24812 52351: contig of 27540 bp in length
52352 52451: gap of 100 bp
52452 62074: contig of 9623 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11116: contig of 11116 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1117 11216: gap of 100 bp 11217 11216: gap of 1203 bp in length 1325 1335: gap of 100 bp 16536 16635: gap of 100 bp 16536 16635: gap of 100 bp 16536 16635: gap of 100 bp 16536 1667: gap of 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536 16536
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contig of 21737 bp in length
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106944: contig of 14210 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157584 157683: gap of 100 bp 157684 183142: contig of 25459 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183143 183242; gap of 100 bp
183243 189149; contig of 5907 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p of 100 bp contig of 8623 bp in length
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/map="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11217. 13252
/note="assembly_fragment"
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70898. 92634
/note="assembly_fragment"
92735. 106944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone end: SP6
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-376M2

Lupublished

2 (bases 1 to 204685)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Shaderson, S., Baldwin, J., Barra, N., Bastien, V., Beda, F.,

Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,

Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S.,

Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzbugh, W., Gage, D.,

Galagan, J., Gardyus, S., Ginde, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Iltev, I., Johnson, R., Jones, C., Kann, L.,

Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,

Levine, R., Lieu, C., Liu, G., Locke, R., Macdonald, P., Marquis, N.,

Mcarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,

McCarthy, M., McEwan, P., McGurk, A., McKernan, C., Menga, V., Morrow, J.,

Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Connor, T.,

O'Nell, D., Ollvar, T.M., Ollver, J., Peterson, K., Plerre, N.,

Stange-Thomann, N., Schjanovic, N., Subramanian, A., Talamas, J.,

Young, G., Zainou, J., Zimmer, A., and Zody, M.,

Plirett, Submission

Direct, Submission
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Homo sapiens chromosome 17 clone RP11-376M2 map 17, *** SEQUENCING
NORGRESS ***, 9 unordered pieces.
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 204685)
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 189149;
                                                                                                                                                                                                                                                                                                   1303 others
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5.2e-26;
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45663 c 44537 g 47593 t
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HTG; HTGS_PHASE1.
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TITLE
JOURNAL
REFERENCE
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JOURNAL
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KEYWORDS
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Nupublished

State 1 to 222779)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,

Boyuslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,

Campoptano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S.,

Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Klein, J., LaRocque, K., Lamacares, R., Landers, T., Lehoczky, J.,

Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,

Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

O'Neil, D., Ollvar, T.M., Oliver, J., Peterson, K., Plerre, N.,

Pisani, C., Pollara, V., Raymon, C., Riley, R., Rogov, P., Rothman, D.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,

Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J.,

Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Wyman, D., Ye, W. J.,

Liepeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker:html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Sequencing vector: M13; M77815; 26% of reads
Sequencing vector: M13; M77815; 26% of reads
Sequencing vector: Plasmid; n/a; 74% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 221849 bases at least Q40
Consensus quality: 222140 bases at least Q30
Consensus quality: 222140 bases at least Q20
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Insert size: 22579; sum-of-contigs
Quality coverage: 18.7 in Q20 bases; agarose-fp
Quality coverage: 15.8 in Q20.
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   sapiens chromosome 15, clone RP11-351M8
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/db_xref="taxon:9606"
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1 (bases 1 to 222779)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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                                       Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
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14799 62250: contig of 47452 bp in length
62251 62350: gap of 100 bp
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101354: contig of 39004 bp in length
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11950 14698: contig of 2749 bp in length
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site: http://www-seg.wi.mit.edu
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                                                                                                                                                                                                                                  Center project name: L9812
                                                                                                                                                                                                                                                             clone name: 376_M_2
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/chromosome="17"
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VECTOR: pCYPAC2
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Riethman, H.C. and Moyzis, R.K.
Integration of telomeric DNA sequences with the human reference
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/note="cosmid end sequence from half-YAC 2183"
162 c 179 g 134 t 2 others
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2 (bases 1 to 644)
Riethman, H.C. and Moyzis, R.K.
Blicet Submission
Submitted (25-JUN-2000) Molecular Genetics, T
3601 Spruce St., Philadelphia, PA 19104, USA
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Homo sapiens clone 15qtel_c320at3 sequence.
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100.0%; Pred. No. 8.6e-26;
iive 0; Mismatches 0;
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100.0%; Pred. No. 5.3e-26;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 68; Conservative
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DERINITION

Himman DNA sequence from Clone REPL-64K7 on Chromosome 2011.12.11.23

CONCERSION

Himman DNA sequence from Clone REPL-64K7 on Chromosome 2012.12.11.123

CONCERSION

MANAGES TREAS (1635 John Paper)

FERSION

MANAGES REPLACE ASBAD PART PARTERIES The gene for wherever an unclear ribonucleoprotein RAIV or automatigen for heterogenous nuclear ribonucleoprotein RAIV or automatigen for heterogenous nuclear ribonucleoprotein RAIV or automatigen for heterogenous nuclear ribonucleoprotein RAIV or automatigen for the gene for the force of the f
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/evidence-not_experimental
/product="dJ64K7.3.2 (heterogenous nuclear
ribonucleoprotein RALY or autoantigen P542, isoform 2.)"
join(15308 . 15390, 55852. . 56116,57349. .57421,59660 . .59826,
60488 . .60601,60814 . .61031,62291 . .62339,63696 . .64047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gener_augua.h.;
//note="continued from.dj1125All.; in Em:AL034549
match: cDNAs: Em:L38696 Em:L17076 Em:S72641
match: EST9: Em:Al040012 Em:AL1278999 Em:AL056329
Em:AL346620 Em:AL30897 Em:AA305550 Em:H46063 Em:AA909993
Em:AL143622 Em:AA309995 Em:AA305550 Em:AA450074
Em:AL15165 Em:AL36010 Em:AL361019 Em:AA4507074
Em:AA135401 Em:AA306995 Em:AA431697 Em:AA445175
Em:AA31642 Em:AA186593 Em:AA431697 Em:AA4451757
Em:AA31642 Em:AA186593 Em:AA4657569 Em:W60816 Em:AA450198
Em:AA31642 Em:AA186593 Em:AA335840 Em:AA35999
Em:AA335913 Em:AA4076509 Em:AA335840 Em:AA35999
Em:AA33591 Em:AA076509 Em:A1335840 Em:AA35999
Em:AA335403 Em:AA076509 Em:A133540 Em:AA35999
Em:AA335403 Em:AA076509 Em:A1345750 Em:AA451033
Em:AA634978 Em:AA076509 Em:A1345750 Em:AA315810
Em:AA634978 Em:AA13315 Em:A156251 Em:AA158591 Em:R73202
Em:AA634978 Em:AA13315 Em:AA43809 Em:T92248 Em:AA281678
Em:AA634978 Em:AA143315 Em:A156251 Em:AA158591 Em:R73202
Em:AA6364978 Em:AA143315 Em:AA43809 Em:T92848 Em:AA281678
Em:AA6364978 Em:AA143315 Em:AA43809 Em:H52643 Em:AA281678
Em:AA646511 Em:A149275 Em:AA2809 Em:AA13364 Em:AA292970
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//Octe="L2 repeat: matches 2514. .2547 of consensus"

14842. .15145

/Anote="Alusg repeat: matches 2. .290 of consensus"

15146. .15251

/Anote="L2 repeat: matches 2547. .2661 of consensus"

15146. .15281

/Anote="L2 repeat: matches 2547. .2661 of consensus"

15160. .15380. .15390,5882. .56116,57349. .57421,57605. .5

5660. .59856. 64047)

// Gene="d464K7.3"

/Anote="d564K7.3"

/Anote-"d564K7.3"

/Anote-"d564K7.3"

/Anote-"d664K7.3"

/Anote-"d664K7.3
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/product="dJ64K7.3.1 (heterogenous nuclear
ribonucleoprotein RALY or autoantigen P542, isoform 1)"
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16453. .16578
/note="MIR repeat: matches 20. .145 of consensus"
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/gene="dd6447.3"
15760. .16048
/note="AluSp repeat: matches 1. .289 of consensus"
16305. .16436
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DEFINITION Homo sapiens chromosome 12 clone RP11-1143G9, WORKING DRAFT
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18657. .18968
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:ive 0; Mismatches
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/note="Aluxa5 repeat: matches 1. .290 of consensus" 4375. .4563

/note="MRS8A repeat: matches 6. .220 of consensus" 4730. .5048

/note="Alusx repeat: matches 1. .312 of consensus" 5059. .5444

/note="MRTD repeat: matches 1. .393 of consensus" 5478. .5529

/note="MRTD repeat: matches 55. .108 of consensus" 5478. .5529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7705. .7810
/note="AluSq/x repeat: matches 1. .103 of consensus"
complement(7840. .8061)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5847. :5878
hote="8 copies 4 mer tctt 93% conserved"
5881. :6014
/note="FLAM_C repeat: matches 1. :133 of consensus"
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                                                             .2744 of consensus"
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note-"FLAM_C repeat: matches 1. .127 of consensus"
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12978. .13245
/note="AluSx repeat: matches 37. .304 of consensus"
                                                                                                                                                                                                                                                                                                             .2691 of consensus"
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/note="MIR repeat: matches 109. .227 of consensus"
complement(7236. .7541)
/note="match: GSS: Em:AQ070626"
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/note-"Alusx repeat: matches 1. .294 of consensus"
9683. .9706
/note-"12 copies 2 mer tt 95% conserved"
10177. .10453
/note-"Alux repeat: matches 43. .311 of consensus"
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/note="MIR repeat: matches 19. .187 of consensus"
11708. .11982
/note="match: GSS: Em:AQ536379"
11796. .12090
                                                                                                                                                                                        consensus
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/note="25 copies 2 mer gg 72% conserved"

13265. 13296

/note="8 copies 4 mer aggg 100% conserved"

13972. 14172

/note="MIR repeat: matches 16. 1228 of consensus"

14397. 14469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7855. .7939
/note="MIR repeat: matches 59. .143 of consensus"
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/note="34 copies 2 mer tt 67% conserved"
                                                                                                                                                                                     Jo
                                                                                                                                                                                     . 298
                                                                                                                                              2827. .3128
/note="AluSx repeat: matches 1.
complement(3014. .3464)
/note="match: GSS: Em:AQ793025"
                                                                                                                                                                                                                                                                                3357. .3479
/note="L2 repeat: matches 2580.
                         1582. .1643
/note="L2 repeat: matches 2682.
1739. .2318
/note="match: GSS: Em:AQ532111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7239. .7541)
/note="match: GSS: Em:AQ070612"
/note="match: GSS: Em:AQ791660"
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/db_xref-"taxon:9606"
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Mammalia; Butherlas; Primates; Catarrhini; Hominidae; Homo.

Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,

Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.,

Benton, J., Binqey, K., Blankenburg, K., Bonnin, D., Bouck, J.,

Burde, S. Briewa, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,

Burde, D., Briewa, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,

Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Chen, G., Chen, R.,

Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,

Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L.,

Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,

Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H.,

Ugan-Rocha, S., Dubbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,

Elbaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagar, N., Ford, J.,

Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,

Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,

Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hane, S.,

Hamilton, E., Jacobson, B., Jida, Y., Johnson, R., Jolivet, S.,

Joudah, S., Karlsson, E., Kelly, S., Khan, U., Korvah, J.,

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Martinez, E., Massey, E., Maxhiney, E., McLed, C., Liu, J., Liu, M.,

Martinez, E., Massey, E., Maxhiney, E., McLed, M. Paton, B.,

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Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S.,

Oudles, M., Morris, S., Massey, E., McChell, T., Spacks, A., Stanley, H.,

Ruz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,

Stson, H., Sutton, A., Syatek, M., Tansey, J., Perca, J., Patca, J., Tamerlisa, R.,

Thomas, S., Usmani, K., Vasquez, L., Vers, V., Villalon, C., Walliams, G., Williams, G., Williams, G., Williams, G., Williams, G., Williams, G.,
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Submitted (08-JAW-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Contact: hgsc-help@bcm.tmc.edu
SEQUENCE, 5 unordered pieces.
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Worley, K.C.
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Unpublished
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Direct Submission

Submitted (22-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
on Feb 16, 2001 this sequence version replaced gi:12830334.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate
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                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Estimated insert size: 149939; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Human DNA sequence from clone RP11-113J24 on chromosome 13,
complete sequence.
                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Best Local Similarity 100.0%; Pred..No. 1.8e-25;
Matches 68; Conservative 0; Mismatches 0;
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11893. .12012
/note="L1MC5 repeat:
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chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, GARLSPROT: Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at RPI1-113124 is from the library RPCI-1111 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is the entire insert of clone RPI1-113J24 The true left end of clone RPI1-153Q23 is at 145239 in this sequence. The true right end of clone RPI1-23J1Z12 is at 41597 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anote="MIR repeat: matches 19. .192 of consensus" 7017. .7182
Anote="MER90 repeat: matches 435. .603 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER58B repeat: matches 20. .336 of consensus"
6616. .6777
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/note="TRR27 repeat: matches 289. .580 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .514 of consensus"
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/note="AluJo repeat: matches 3. .289 of consensus"
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/note="LTR28 repeat: matches 1. .178 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note-"Alusx repeat: matches 1. .293 of consensus"
11079. .11120
note-"MLTIF repeat: matches 469. .514 of consensus
11093. .11125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .292 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             matches 1. .297 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .70 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .249 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MSTA repeat: matches 1. .426 of consensus"
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/note="MLTIF repeat: matches 481.
11139. .11438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2881. .3186
/note="AluYa5 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121. .8192
note="LTR1 repeat: matches 119.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307. .luyo
/note="AluSg repeat: matches 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="RPCI-11.1"
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/note="AluJb repeat:
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/note="CpG island"
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76907. 27197 Anote—"Alusp repeat: matches 1. 292 of consensus" 27557. 27610 Anote—"Alusp repeat: matches 1. 292 of consensus" 27557. 27610 Anote—"27 copies 2 mer aa 77% conserved" 27631. 27785 Anote—"MIR repeat: matches 52. 216 of consensus" 28187. 28189 Anote—"Alusg repeat: matches 2. 30% of consensus" 28510. 29511 Anote—"LiPalo repeat: matches 1. 286 of consensus" 2812. 29572 Anote—"LiPalo repeat: matches 5715. 6156 of consensus" 2972. 29559 Anote—"LiPalo repeat: matches 1. 288 of consensus" 29560. 30186 Anote—"LiPalo repeat: matches 5715. 5715 of consensus" 29590. 30186 16383. .16681

// note="AluSx repeat: matches 1. .299 of consensus 201295. .20591
// note="AluSx repeat: matches 2. .299 of consensus" 201295. .20591
// note="AluSx repeat: matches 2. .299 of consensus" 22740. .22783
// note="MIR repeat: matches 98. .153 of consensus" 22856. .22911
// note="MIR repeat: matches 98. .153 of consensus" 24655. .24799
// note="MERSA repeat: matches 1. .306 of consensus" 24675. .24799
// note="MERSA repeat: matches 61. .186 of consensus" 25712. .25753
// note="21 copies 2 mer ac 97% conserved" 25712. .25753
// note="10 copies 4 mer acac 100% conserved" 26029. .26422
// note="10 copies 4 mer acac 100% conserved" 26029. .26422
// note="11 MAY repeat: matches 5872. .6294 of consensus" 26029. .26422 .2747 of consensus" /note="AluSx repeat: matches 1. .302 of consensus" 12980. .13289 .2399 of consensus" // note="L2 repeat: matches 2336. 2399 of consensus 14351. 14443 // note="Mex20 repeat: matches 6. 213 of consensus" 14657. 14808 // note="L2 repeat: matches 2579. 2747 of consensus // note="L2 repeat: matches 2579. 2747 of consensus // note="MIR repeat: matches 23. 169 of consensus 15152. 15461 // note="Aludb repeat: matches 1. 312 of consensus" // note="Aludb repeat: matches 1. 312 of consensus" 'note="AluJb repeat: matches 1. .296 of consensus" of 26818. .26905 /note="44 copies 2 mer cc 67% conserved" 26826. .26905 /note="20 copies 4 mer tccc 81% conserved" 26907. .27197 7794 7670. matches

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/note="LiPA3 repeat: matches 6081. .6146 of consensus" 36303. .36589
/note="AluSx repeat: matches 3. .289 of consensus" 36700. .36725
/note="13 copies 2 mer tt 96% conserved" 37430
/note="AluY repeat: matches 1. .311 of consensus" 37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. .37619. 
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| 0.7 416 16 0.7 650 11 0.7 414 16 0.7 552 14 0.7 860 15 | 0.7 421 150 150 150 150 150 150 150 150 150 15 | 0.6 318 11 0.6 420 14 0.6 4372 21 0.6 372 21 0.6 374 4 | 158 0.6 526 145 BF196304 157 0.6 228 114 AW296524 157 0.6 317 171 BF961941 157 0.6 493 118 AW575677 157 0.6 553 148 BF434169 156 0.6 354 170 BF872931 155 0.6 726 144 BF102508 | 0.6 370 14 0.6 677 13 0.6 754 13 0.6 906 15 0.5 157 17 0.5 278 12 | ALIGNMENTS | 523 bp mRNA _CGAP_Ov18 Homo sapiens | BF116134.1 GI:10985610 BF116134.1 GI:10985610 LST. human. HOmo sapiens Bukaryota, Metazoa, Chordata, Craniata | 1 (bases 1 to 523) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index | Unpublished (1997) Contact: Robert Strausberg, Ph.D. Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.ih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center | Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LINL, send email to: info@inage.linl.gov Seq primer: -40UP from Gibco High quality sequence stop: 479. High quality sequence stop: 479. I523 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="ILMAGE:3570706" /clone="ILMAGE:3570706" |
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Contact: Robert Strausberg, Ph.D.
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mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 518)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Best Local Similarity 100.0
Matches 521; Conservative
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/organism="Homo sapiens"
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Mashington University
Genome Sequencing Center
Clone distribution: NCI-CCAAP clone distribution information can b
found through the I.M.A.G.E. Consortium/LLNL, send email to:
Info@lingel.lnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 493.
Location/Qualifiers
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306 CTTGCTGGTAGAAGATGAAGAGCACGACCAGGAGGCAGCTCAGGATAGGTGGTATA 247
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAhol sites using the following 5' adaptor: GCACGAG(G). Size-selected 5500bp for average insert size 1:8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM52 row: n column: 14
High quality sequence start: 22
High quality sequence stop: 756.
Location/Qualifiers
1. 975
                                                        BE250412 975 bp mRNA EST 13-JUL-2000 600943455T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960077 3'
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NIH-MGC http://mgc.ncl.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-remail.nlh.gov
Tissue Procurement: ATCC
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/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:2932185"
/clone=lib="Soares_NFL_T_GBC_SI"
/clone=lib="Soares_NFL_T_GBC_SI"
/clone=lib="Soares_NFL_T_GBC_SI"
/clone=lib="Soares_NFL_T_GBC_SI"
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_!: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_CCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries The pools consisted of I.M. A.G.E. Clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Qy 25938 ctcctgtccagggagctggcaggcggcctggaggatggggagcctcagcagaagcgggcc 25997
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                                                                                                                     1 (bases 1 to 531)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco
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hf17h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2932185 3', mRNA sequence.
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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SM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (Dases 1 to 456)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Len,V., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M.,
T., Waterston,R. and Wilson,R.
WashUnderck ETP project 1997
Contact: Wilson RK
WashUnder (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 456.
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2v39b08.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone
IMAGE:755991 5', mRNA sequence.
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                                                                                                                                                                                                                                           26088 gcacgcacccgtatctgccctccttgctggtagaagctgaagagcacggtccccaggag
                                                                                                                                                                                                                                                            26148 gcagctcaggataggtggtatggagctgtgccgaggcttggggctcccacataagcactag
                                                                                                                                                                                                                                                                                                                              319 GCAGCTCAGGATAGGTGGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAG
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                                 Length 499;
                                                                   Indels
                                 ; DB 117;
2.6e-140;
                                                                   0; Mismatches
                                 Score 448;
Pred. No. 2
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                                 Query Match 1.7
Best Local Similarity 99.8
Matches 498; Conservative
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//lone_lib="soares_NFL_T_GBC_SI"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_l: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399, subtraction by Bento
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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 26117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -4/UVP from Gibco
High quality sequence stop: 470.
Location/Qualifiers
                                                                03-MAR-2000
   actcagaaggetgtgtgtcttctgccccacgcacgcacccgtatctgccctccttgctgg
                AW510825 499 bp mRNA EST 03-M2
hd40b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2911965 3', mRNA sequence.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2911965"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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AW510825.1 GI:7148903
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Best Local 3
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 478)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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hf45a09.x1 Soares_NFL_T.GBC_S1 Homo sapiens cDNA clone
IMAGE:2934808 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCACAGCTGGGGAATGTCTTTTGGGCTAACTGCCACTCTGTTGTTGTCCTCTATCGAAGT
                                                                                                                                                                                                            Length 456;
              /organism="Homo sapiens"
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                                                                                                                                                                                                          1.6%; Score 439; DB 7; Le
100.0%; Pred. No. 2.8e-137;
iive 0; Mismatches 0;
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Location/Qualifiers
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439; Conservative
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Best Local S
Matches 439
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone=lib="Soares_NFL_T_GBC_SI"
/clone_lib="Soares_NFL_T_GBC_SI"
/clone_lib="Soares_NFL_T_GBC_SI"
/lab_host="DH10B"
/clone=lib="Soares_NFL_T_GBC_SI"
/note="Organ: pooled; Vector: pr773D-Pac (Pharmacia) with
a modified polylinker; Site_l: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbH139v, testis NHT, and B-cell
NCI_CGAP_GCBI) were mixed, and as circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
132 c 122 g 132 t
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LOCUS AIO89646 527 bp mRNA EST 18-AUG-1998
DEFINITION qb16g07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
Tumor Gene Index
Unpublished (1997)
Contact: Nobert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -400P from Gibco
High quality sequence stop: 451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359
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Similarity 99.8%; Pred. No. 1.4e-132;
75; Conservative 0; Mismatches 1;
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48

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AQ218458 525 bp DNA GSS 19-SEP-1998 HS_3247_B1_C06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247 Col=11 Row=F, DNA sequence.
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
7e1: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                         12 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 1.6%; Score 414; DB 225;
Similarity 100.0%; Pred. No. 7e-129;
14; Conservative 0; Mismatches 0;
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Class: BAC ends
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                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 527)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 463.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                527 CTCCTGTCCAGGGAGCTGGCAGGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCC 468
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/db_xref="taxon:9606"
/clone="IMAGE:1696476"
/clone_lib="Soares_pregnant_uterus_NbHPU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 425; DB 16;
Pred. No. 1.4e-132;
0; Mismatches 2;
                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
IMAGE:1696476 3', mRNA sequence.
AI089646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/lab_host="DH10B"
                                      AI089646.1 GI:3428705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="female"
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99.68;
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1 (bases 1 to 478)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: nervous_normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-201200-574-d07&t3=2000-12-20&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 478.
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                                                                                                                                                                                                                                          BF963225 478 bp mRNA EST 22-JAN-2001
QV2-NN0045-201200-574-d07 NN0045 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                              \operatorname{Simpson}, A . J. Shotgun sequencing of the human transcriptome with ORF expressed
   aagagctgtgtttctgggaagaccactatctgggtttacagttcagaggccggcactcct 14002
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Pred. No. 1.6e-128;
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/db_xref="taxon:9606"
/clone_lib="NN0045"
/dev_stage="Adult"
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99.8%;
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Fax: +55-11-2707001
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Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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/db_xref="taxon:9606"
/db_are_lib="NN0045"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: pucl8; Site_1: Smal;
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV2&t2=QV2-NNOO45-
051200-516-d05&t3=2000-12-05&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 504.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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HS-1059-A1-G03-MR.abi CIT Human Genomic Sperm Library C Homo
sapiens genomic clone Plate=CT 781 Col=5 Row=M, DNA sequence.
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Pred. No. 3.4e-127;
0; Mismatches 1; Indels 0;
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    Sequence Tagged Connector

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Matches 459; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 673)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

        901
        gagctgaaacccagccccagcatcgacatgggcatcttgtggcaagagctgtgtttctggg
        13960

        94
        GAGCTGAAACCCAGCCCAGCATCGACATCTTGTGGCAAGAGCTGTTTCTGGG
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602449690F1 NIH_MGC_14 Homo sapiens CDNA clone IMAGE:4588007
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Pred. No. 7.4e-127;
0; Mismatches 1;
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                                                                                          /organism="Homo sapiens"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
Plate: CT 781 row: M column:
                                                                                                           /db_xref="taxon:9606"
             Class: BAC ends
High quality sequence stop: 4
Location/Qualifiers
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SOURCE
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FEATURES

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Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
                         Vertebrata; Euteleostomi;
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=3213 Col=2 Row=N"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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                                                                                                                                                          Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                               , Wallace, J.C., Smith, K., Swartzell, S., Holzman, T
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601274815F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615939 9
mRNA sequence.
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                         Craniata; Vertebrata; E
Catarrhini; Hominidae;
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Exex: (206) 616-3887
Email: jwallace@u.washington.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3213 row: N column: 2
Class: BAC ends
High quality sequence stop: 511.
Location/Qualifiers
                       Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
1 (bases Lt o 511)
Mahairas, G.G., Wallace, J.C., S
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/ Organism="Homo sapiens"

/ db_xref="taxon:9606"

/ clone="Inb="NIH_MGC_14"

/ tissue_type="reni cell adenocarcinoma"

/ tissue_type="reni cell adenocarcinoma"

/ lab_host="DH10B (phage-resistant)"

/ lab_host="lab_host="lab_host-resistant)"

/ lab_host="lab_host-resistant)"

/ lab_host="lab_host-resistant)"

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K3.3213_B2_G01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Co1=2 Row=N, DNA sequence.
AQ175652
AQ175652. GI:3573019
GSS.
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                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1319 row: d column: 24
High quality sequence stop: 672.
Location/Qualifiers
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1. 627

/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:3615939"
/clone=InAGE:3615939"
/clone=InAGE:3615939"
/clone=InDist="DHIOB (phage-resistant)"
/lab_lbost="DHIOB (phage-resistant)"
/note="Organ: skin: Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500b for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC tolone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM280 row: n column: 04
High quality sequence start: 18
High quality sequence stop: 611.
Location/Qualifiers
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                                                                                                                                                            NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 CTTGCTGGTAGAAGCTGAAGAGCACGGTCCCCCAGGAGGCAGCTCAGGATAGGTGGTATG 532
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                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 440)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli, B., Chisoe,S., Dietrich,N., Duebuque,T., Favello,A., Gish,W., Hawkins,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Generation and analysis of 280,000 human expressed sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1829 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 418.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA410664 440 bp mRNA EST 08-AUG-1997 zt29g11.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:723812 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="Soares ovary tumor NDHOT"
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100.0%; Pred. No. 1.2e-107;
tive 0; Mismatches 0;
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/db_xref="GDB:5935201"
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88 c 92 q
                                                                                         AA410664.1 GI:2069769
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351; Conserv
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26124 ctgaagagcacggtcccccaggaggcagctcaggataggtggtatggagctgtgccgagg 26183
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AW407520/c
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                    AA811170 396 bp mRNA EST 19-FEB-1998 ob42c03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1334020 3',
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 396)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
14217 ttacctgcattgaaacaaatgaggtgggtcagagtgtgtgagactgtcgtggtcaagagt 14276
                                                                      ccgtgttatgggatggactcacagctggggaatgtcttttgggctaactgccactctgtt 14336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                      219 TTACCTGCATTGAAACAAATGAGGTGGGTCAGAGTGTGTGAGACTGTCGTGGTCAAGAGT 160
                                                                                       /tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 885 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 377.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                      AA811170
AA811170.1 GI:2880781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
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                                                                                                                                                                                                                                                                                                         mRNA sequence.
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AA811170/c
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VERSION
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AUTHORS
TITLE
                                                                    14277
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SOURCE
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/cell_tibe="mcG8"
/constructed from size fractionated cytoplasmic mRNA
(2.5-3.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbr/image/image.html

Seq primer: MI3 Forward.
                                                                                                                                                                                                                                         1 (bases 1 to 345)
NIH-MGC http://mgc.ncl.nih.gov/.
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW407520 345 bp mRNA EST 16-FEB-2000 UI-HF-BM0-adl-b-07-0-UI.I1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3061957 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 TCCCTGCACACCCAGAGACAAGCAGAGTAACAGGATCAGTGGGGTCTAAGTGTCCGAGACTT 56
                                                                                         cttggggctcccacataagcactagtctatagatgcctcttaggactggtgcctggcacag
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ORIGIN
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1.3%; Score 338; DB 115; Length 345;

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Gaps

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Length 396; Indels

1.3%; Score 343; DB 12; I 100.0%; Pred. No. 5.9e-105; Live 0; Mismatches 0;

Best Local Similarity 100. Matches 343; Conservative

Query Match

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derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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Unpublished (1998)
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AUTHORS
TITLE
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1 (bases 1 to 475)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=CM2&t2=CM2-NN1145-
230900-384-b08&t3=2000-09-23&t4=1)
Seq primer: puc. 18 forward
High quality sequence start: 14
High quality sequence stop: 473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A min1-library was made by cloning products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens cDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                              aagagcacggtcccccaggaggcagctcaggataggtggtatggagctgtgccgaggctt 26186
                                                                                                                             gggctcccacataagcactagtctatagatgcctcttaggactggtgcctggcacagccg 26246
                                                                                                                                                                                            cgggccaggaggctgccacacggaagcaagcagatgaactaatttcatttcaaggcagtt 26306
                                                                                                                                                                                                                                                        26307 tttaaagaagtettggaaacagacggcgcacettteetetaatecagcaaagtgattee 26366
                                                                                                                                                                                                                                                                                                                         ctgcacaccagagaccagagcagagtaacaggatcagtgggtctaagtgtccgagacttaac 26426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                             226
                                                                              106
                               Gaps
                                                                                                                                                                                                                                                                                                                                         24-NOV-2000
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20202663
                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3e-103;
Mismatches 0;
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CM2-NN1145-230900-384-b08 NN1145 HOMO
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100.08; FE
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BF364978.1 GI:11327003
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                              338; Conservative
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               Similarity
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Bonaldo, Ph.D. cDM Library Arrayed by: Greg Lennon, Ph.D. DNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A1937465 531 bp mRNA EST 08-MAR-2000 wp77e01.xl NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467800 3',
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 531)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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  Length 475;
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1.2%; Score 328; DB 147;
llarity 99.5%; Pred. No. 6.2e-100;
Conservative 0; Mismatches 2;
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1. .584
/organism="Homo sapiens"
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/cell_line="NT2"
                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                         Helix Research Institute.
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AU138595
AU138595.1 GI:11000116
   AU127299.1 GI:10952015
                                                                                                    HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
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AU138595 PLACE1 Homo
                                                                                             Isogai, T.
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                                                                                                                                                                                                                                                              Score 325; DB 103; Length 531;
Pred. No. 6.1e-99;
0; Mismatches 4; Indels 0;
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/organism="Homo sapiens"
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/lab_host="DH10B"
    at:
found through the I.M.A.G.E. Consortium/LLNL, www-bio.llnl.gov/Abrp/image/image.html
Insert Length: 1291 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 467.
Location/Qualifiers
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al Similarity 99.2%;
525; Conservative
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/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction" 166 c 178 g 115 t 3 others
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Helix Research Institute
153.2 *Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5.* 6 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and
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Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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                                               Catarrhini; Hominidae; Homo.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Best Local Similarity 100.0%; Pred. No. 1.3e-97;
Matches 321; Conservative 0; Mismatches 0;
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94
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                                              Euteleostomi;
                                                                                                                                                                                                                                                  Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of '
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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AA676661 GI:2657183
                                                                      1 (bases 1 to 696)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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                                                          Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                              Vertebrata;
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
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Pred. No. 5.8e-97;
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                                            Eukaryota; Metazoa; Chordata; Craniata;
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/tissue_type="placenta"
/note="Vector: pME185FL3"
a 192 c 208 g 130 t
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/db_xref="taxon:9606"
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                                                                                                                                  HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pac I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 491). Howels, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., WashG-NI, human EST Project
Uppublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
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Washington University School of Medicine
4444 Porest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 from Amersham.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:459985"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/sex="male"
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Best Local Similarity 99.33
Matches 452; Conservative
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6430

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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?t1=IL5&t2=IL5-IT0026-
151100-261-b06&t3=2000-11-15&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 332.
1. 346
                                                                                                                                                                                                                                                                                                                                                                BF769772 346 bp mRNA EST 12-JAN-2001
IL5-IT0026-151100-261-b06 IT0026 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 346)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                          gcacccagcaaaggccagagaagtccagaacctggcgaggagatgaggcttacactgact 6321
                                                                                                                                                 251 CCTTGTTAGTACTAACTAATGTGATGCTTACCAAGTAGTGCTGATGGGTGACAGACCAGA 310
                                                                gaaggcagaaggcagcagggaggaggaatgtgccggagcaatggcacaagtgctccta
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20202663
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BF769772.1 GI:12117672
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AUTHORS
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BF769772
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                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 514)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivelra, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-131100-414-e12&t3=2000-11-13&t4=1)
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                                                                                                                                                   BF954354 514 bp mRNA EST 22-JAN-2001
QV2-NN0045-131100-414-e12 NN0045 Homo sapiens CDNA, mRNA sequence.
BF954354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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ilarity 99.7%; Pred. No. 7.4e-90;
Conservative 0; Mismatches 1;
                 Qy 26430 aatagtatttcagctgcaataaagattgagtttgc 26464
                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0045"
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High quality sequence stop: 476.
Location/Qualifiers
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                                                                                                                                                                                                                                 BF954354.1 GI:12371629
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Best Local S
Matches 348
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="IT0026"
/dev_stage="Adult"
/note="Organ: epid_tumor; Vector: puc18; Site_l: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
15 a 72 c 94 g 105 t
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Pred. No. 8.7e-89;
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1 (bass 1 to 343)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Soldan, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpsoneludwig.org.br
Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?tl=CM4&t2=CM4-HN0020-181100-444-a09&t3=2000-11-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 27
High quality sequence stop: 343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF825929 343 bp mRNA EST 13-JAN-2001
CM4-HN0020-181100-444-a09 HN0020 Homo sapiens cDNA, mRNA sequence.
BF825929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                          \operatorname{Simpson}, \operatorname{A}.\operatorname{J}. Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                     tcaacctgacagttacctgtttaggtatccacaaagagaccagaagggtgttgatggtga 13617
                                                                                                                                                                                                                                           tgtgtaaagttggttttgtgctttgtttacctctcagctcactggataggatatgtcatg 13677
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                                                                                                                                                                                                                                                                           61 TCAACCTGACAGTTACCTGTTTAGGTATCCACAAAGAGACCAGAAGGGTGTTGATGGTGA 120
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing by: Washington University Genome Sequencing by: Washington University Genome Listribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: infofalmage.llnl.gov
Seq primer: -40DP from Gibco
High quality sequence stop: 493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE858252 494 bp mRNA EST 29-SEP-2000
7g2la09.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3307096 3',
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 494)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

(Dipublished (1998)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                       18204 gaccattgacccctcagaggacatttggcaacatctggaaacgttcttggttgtcacagc 18263
                                                                                                                                                                                                                                                                                                                                                       18383
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                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 GCCCTGAGGCAGAGCGATGCAGCATCCAAAAGGCGGTGGAGCAGACCTGCCCCAGATCCT
                                                                                                                                                                                      343 GACCATTGACCCCTCAGAGGACATTTGGCAACATCTGGAAACGTTCTTGGTTGTCACAGC
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0
                    Length 343;
                                                                     Indels
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/clone="twade:33070906"
/clone="twade:33070906"
/tissue_type="glioblastoma (pooled)"
                    DB 170;
                                           8.9e-88
1.1%; Scc. 100.0%; Pred. No. ... 0; Mismatches
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RESULT 29
AI803400/c
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T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatina Bonaldo."
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Other ESTs: 2820640.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
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Homo sapiens cDNA clone IMAGE:2820640 3',
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                                                                                                                  Score 290; DB 141; Length 494;
Pred. No. 3.7e-87;
0; Mismatches 4; Indels 0
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2820640.3prime NIH_MGC_7 HG
mRNA sequence.
AW248468 AW248468.1 GI:6591461
                                                                                                                  1.1%;
Similarity 99.2%;
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Best Local
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LOCUS
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI803400 489 bp mRNA EST 13-DEC-1999 tc42f03.x1 Soares_totel_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2067293 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                  214 GCCACACGGAAGCAAGCAGATGAACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCAT 155
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                                                                                                                                                                                                                                                                            Length 394;
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Pred. No. 4.2e-85;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                            1.1%;
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Best Local Similarity 99.5
Matches 384; Conservative
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69 AGTGGGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAG 10
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                                                                                                                                    Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This Consortium (info@image.llnl.gov) for further information.
Insert Length: 1275 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 446.
                                                          1 (bases 1 to 489)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 ATCTGCCCTCCTTGCTGGTAGAAGCTGAAGAGCACGGTCCCCCAGGAGGCAGCTCAGGAT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCATGGAAACAGACGGCGGCACC 130
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Pred. No. 8.4e-85;
0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                        Homo sapiens
Eukaryota; Metazoa;
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CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Glound through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 680 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 336.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anotes Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was prepared from I2 pooled bulk tumor samples amples and primed with a Not I - 0.130(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of mornal ization.
                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 489)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                       EST 21-AUG-1997 sapiens CDNA clone IMAGE:925867 3',
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Pred. No. 4e-84;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:925867"
/clone_lib="NCI_CGAP_Co3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH108"
                                                                                                                                                                       AA534478 489 bp mRNA nf76f10.s1 NCI_CGAP_CO3 Homo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 670)
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Contact: Takeo isogai

Contact: Takeo isogai

Contact: Takeo isogai

Genomics Laboratory

Helix Research Institute

133.2 *Y ana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3951

Fax: 81-438-52-3952

Fax: 81-438-
                                                                                                                                                                                                                                  gaactaatttcatttcaaggcagtttttaaagaagtcttggaaacagacggcggcactt 26341
                                                                                                                                                                                                                                                                                                                                     gtggtatggagctgtgccgaggcttgggctcccacataagcactagtctatagatgcctc 26221
                                                                                                                              Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                         GAACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCATGGAAACAGACGGCGGCACCTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU143668 670 bp mRNA EST 25-OCT-2000 AU143668 Y79AA1 Homo sapiens CDNA clone Y79AA1002297 5', mRNA
                                                   305 GIGGTATGGAGCTGTGCCGAGGCTTGGGGTCCCACATAAGCACTAGTCTATAGATGCCTC
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190 c 193 g 127
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Location/Qualifiers
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//crganism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="INAGE:458124"
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/tissue_type="retinoblastoma"
/lab_host="Data" Shide_1: xhoI; Site_2:
FCORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGGG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

En (Dases 1 to 746)

In (Dases 1 to 746)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Longublished (1999)

Longublished (1999)

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Arcc

CONA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM1301 row: k column: 05

High quality sequence stop: 741.
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BG395840 746 bp mRNA EST 12-MAR-2001
6024588622F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4581244 5′,
mRNA sequence.
BG395840
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                                                                                                                                               ggcgccgcgctctacgtcttctccgagttcaaccggt 1156
                                                                                                                                                                                   241 GGCGCCGCCTCTACGTCTTCTCCGAGTTCAACCGGT 277
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 666)
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                              Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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                                                                                                                                                                      1.0%; Score 276; DB 10; Length 461; 99.7%; Pred. No. 1.9e-82; ive 0; Mismatches 1; Indels (
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/db_xref="taxon:9606"
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Location/Qualifiers
1. .666
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AU141334
AU141334.1 GI:11002855
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                    Best Local Similarity 99.7
Matches 326; Conservative
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Hillar, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marta, M., Martin, J., Moore, B., Schellenberg, K., Steptce, M., Tan, F., Theising, B.,
Washle, Y., Wylie, T., Waterston, R. and Wilson, R.
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
444 Forest Parkway, Box 8501, St. Louis, Mo 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 694 Std Error: 0.00
Seq primer: -28m13 revl Er from Amersham
High quality sequence stop: 453.
Location/Qualifiers
                                                                                                           361
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ab48b06.rl Stratagene lung carcinoma 937218
IMAGE:844019 5', mRNA sequence.
AA635046.1 GI:2558260
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/clone="IMAGE:844019"
/clone_lib="Stratagene lung carc/tissue_type="lung carcinoma"
/cell_line="NoI-H69"
/dev_stage="cell line NCI-H69"
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/organism="Homo sapiens"
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Best Local Similarity
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1 (bases 1 to 53)
1 (bases 1 to 54)
1 (bases 2 to 54)
1 (bases 3 to 54)
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be set in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=MR2&t2=MR2-CI0128-071200-011-e04&t3=2000-12-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 532.
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MR2-C10128-071200-011-e04 C10128 Homo sapiens cDNA, mRNA sequence.
BF816722
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \operatorname{Simpson}, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
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20202663
                                                                                                                                                                                                          Length 666;
                                                                                                         3 others
                                                                                                                                                                                                        1.0%; Score 274; DB 108;
100.0%; Pred. No. .8.1e-82;
tive 0; Mismatches 0;
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/clone="THYRO1000421"
/clone_lib="THYRO1"
/tissue_type="thyroid gland
/note="vector: pME18SFL3"
a 186 c 190 g 129 t
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                       274; Conservative
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/clone_lib="CIO18"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: colon_ins; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pucl8 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21378 attgccaccttgcctccgcctcccgactccttttcccccagaaggtaatgtcttagcac 21437
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BG253351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 ACTGCACAGCAGAATAGCCCAAGAAGTTTGTCAGAATCCAGACTTCCAGAGCCCTGCCTA 106
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1 (bases 1 to 742)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                                                                                                                                Length 533;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                Score 273; DB 169;
Pred. No. 1.9e-81;
O; Mismatches 4;
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Best Local Similarity
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COMMENT
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                                            AUTHORS
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                                                                        TITLE
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                                                                                                                            /clone="IMAGE:411427"
/clone="IMAGE:411427"
/clone_lib="NIH_MGC_90"
//tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

194 c 221 g 136 t
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 distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                           1.0%; Score 269; DB 175; Length 742; 99.4%; Pred. No. 3.7e-80; live 0; Mismatches 2; Indels 1.
Clone distribution: MGC clone accounting/LiNL at found through the I.M.A.G.E. Consortium/LiNL at
                          http://image.llnl.gov
Plate: LLAM10290 row: k column: 12
High quality sequence stop: 682.
Location/Qualifiers
                                                                                    1. 742
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                        Mewes, H.W., Gassenhuber, J. and Wiemann
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                       AM. Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKP2); Email s. wiemann@dkfz- heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
Is sequence also available.
Is sequence also available.

Inis clone (DKF2p434B2311) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
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AU126037 NT2RM4 Homo sapiens CDNA clone NT2RM4002610 5', mRNA
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62 c 63 g 170 t 5 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="44 (synonym: htes3)"
/clone_lib="434 (synonym: htes3)"
/clssue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 268; DB 105;
Pred. No. 9.7e-80;
0; Mismatches 1;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                        Duesterhoeft, A., Lauber, J.,
                                                                                                                       EST (Duesterhoeft, et al.)
                                                                                                                                          Unpublished (1999)
Contact: Duesterhoeft A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AU126037
AU126037.1 GI:10950753
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99.78;
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                  /cell_type="teratocarcinoma"

/cell_line="NT2"

/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells:
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                                                  Isogai,T.

Har human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamanoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute
1532-3 Tana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 727)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                               Email: genomicseni.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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                      Ota'T', Wakamatsu'A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG166177 727 bp mRNA EST 06-FEB-2001
602340918F1 NIH_MGC_89 Homo sapiens CDNA clone IMAGE:4448596
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 8.2e-80;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                         134
                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM4002610"
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268; Conservative
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           REFERENCE
AUTHORS
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COMMENT
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rissue procurement: Arc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10231 row: d column: 05

High quality sequence stop: 709.

Location/Qualifiers

1. 727

/organism="Homo sapiens"

/drawnism="Homo sapiens"

/drawnism="Homo sapiens"

/drawnism="HAGS: 4448396"

/clone="IMAGS: 4448396"

/clone="IMAGS: 4448396"

/lasue=Lyppe="hypernephroma, cell line"

/lab_host="H9H108" (phage-resistant)"

/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: Sall; cloned unidirectionally; oligo-df primed.

Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.

Note: this is a NHH_MGC Library."
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AU138795 PLACE1 Homo sapiens CDNA clone PLACE1009311 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gggcggccctcctgtccagggagctggcaggcggcctggaggatggggagcctcagcaga
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Pred. No. 3.9e-78;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 t
                        Ph.D.
Unpublished (1999)
Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 g
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I 3']; double-stranded cDNA was ligated to Eco RI addedors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library is normalized, and was constructed by Bento
                                                                                                                                                                                       Sequencing Center
information can be
                                                                                       Email: cgapbs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2499 Std Error: 0.00
Seq primer: -40UP from Giboo
High quality sequence stop: 351.
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BF309436.1 GI:11256824
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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100.0%; Pred. No. 2.4e-77;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soares and M.Fatima Bonaldo."
                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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Matches 261; Conserva
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TITLE
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BF309436
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 356)
                                                        Homo sapiens
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 657)
                                                                                                                                                                                                                                                                                                                                   Email: genomicsehri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute
                                                                                                                             Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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                                                                                                                                                                                                   Unpublished (2000)
Contact: Takko Isogai
Genmics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Fax: 81-438-52-3951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.0%; Score 262; DB 108;
100.0%; Pred. No. 8.9e-78;
tive 0; Mismatches 0;
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/note="Vector: pME18SFL3"
176 c 192 g 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .657
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="PLACE1009311"
/clone_lib="PLACE1"
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                                                                                                                                                                                     human cDNA project
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   REFERENCE
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                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="rhabdomyosarcoma"
/tab.host="DH10B (phage-resistant)"
/note="Organ: muscle: Vector: poTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dr priming.
Site_2: XhoI; cDNA made by oligo-dr priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1045 row: h column: 07
High quality sequence stop: 457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   956 tgtcgcagggacgcaccatatcgcaggcacccgccgcggagcggcggcgaaggacc 1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1016 cgctgcggcacctgcgcacgcgagagaagcgcggaccgtcgggggtgctccggcggcccaa 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        896 giggagacgogcaigtgggcgcittgcicgcigcigcggiccgcggacgcacca 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                   NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0%; Score 261; DB 147; Length 457; 100.0%; Pred. No. 2.2e-77; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4137654"
/clone_lib="NIH_MGC_17"
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:3254061
                                      (bases 1 to 457)
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AI033108.1
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TITLE
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/organism="Homo sapiens"
/do_zerf="texton:9606"
/clone="InhAGE:1654910"
/clone="InhAGE:1654910"
/clone="InhAGE:1654910"
/clone="InhAGE:1654910"
/dev_stage="20 week-post conception fetus"
/dev_stage="20 week-post conception fetus"
/dev_stage="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
with a modified polylinker; Site_1: pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - oligodI) primer [5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                  Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length. 773 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 368.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 AGAAGCTGAAGAGCACGGTCCCCCAGGAGGCAGCTCAGGATAGGTGGTATGGAGCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 GTGATTCCCTGCACACAGGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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hf4la01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 410;
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Pred. No. 2.4e-75;
0; Mismatches 3;
                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0%;
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DEFINITION
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FW10165"
/dev_stage="Adult"
/note="Organ: prostate_normal; Vector: pucl8; Site_1: SmaI
/site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196/716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
                                                                                                                                                                                                                                                                                       Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 359)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magal,M.A., Bordin,S., Costa,F.F.,

Nagal,M.A., da Silvay,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M. Sares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=RC6&t2=RC6-FN0165-
180700-011-GG7&t3=2000-07-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 51
High quality sequence stop: 358.
Location/Qualifiers
                                                                                                                                                  BF371674 359 bp mRNA EST 24-NOV-2000
RC6-FN0165-180700-011-G07 FN0165 Homo sapiens CDNA, mRNA sequence.
BF371674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy 14638 tccagttttgggcagcaaaacctcttcaatgaatcaggtgtcatttgagagccatgtgtg 14697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 TCCAGTTTTGGGCAGCAAAACCTGTTCAATGAATCAGGTGTCATTTGAGAGCCATGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                       26428 aaaatagtatttcagctgcaataaagattgagtttgcaa 26466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 254; DB 147;
Pred. No. 5.4e-75;
0; Mismatches 1;
                                            41 AAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTGCAA 3
                                                                                                                                                                                                                               BF371674.1 GI:11333699
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SOURCE
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/db.xref="Taxon:960"
/clone="IMAGE:2934408"
/clone="IMAGE:2934408"
/clone="Lib="Soares_KFL_T_GBC_S1"
/lab_host="DH108"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbH119W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Pollowing HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731339. Subtraction by Bento
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                                                                                                                           Euteleostomi;
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 461) NCI-GGAP http://www.ncbi.nlm.nih.gov/nciogap. National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
                                                                                                                                                                                                                                        ggctcccacataagcactagtctatagatgcctcttaggactggtgcctggcacagccgc 26247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26068 ctgtgtgtcttctgccccacgcacgcaccgtatctgccctccttgctggtagaagctga 26127
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                                                                                                                                                                                                                                                                                                                                                                                                                1. .461
/organism="Homo sapiens"
IMAGE:2934408 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 g
                                          AW592223.1 GI:7279399
                                                                                                                                                                                                                               Tumor Gene Index
                                                                                                      Homo sapiens
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                                                                                   human.
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//deb_host="DH10B (ampicillin resistant) (also debended by the last stream additional and last stream and resistant and resistant and resistant additional resistant additional resistant additional resistant additional resistant additional resistant 
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[ (bases 1 to 479)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,M., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Wahite,Y., Wylie,T., Waterston,R. and Wilson,R.

Contact: Wilson RR
                                                                               aactggagggaaacacatcagcatgttagtaagtggtctgttgtccaggtggtgaaattt 14817
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 462.
AA716607 479 bp mRNA EST 29.DEC-1997
2g68g07.sl Soares_fetal_heart_NbHH19W Homo sapiens CDNA clone
IMAGE:398556 3', mRNA sequence.
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/db_xref="GDB:1306379"
/db_xref="taxon:9606"
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/dev_stage="19 weeks"
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Score 253; DB 11; Length 479; Pred. No. 1.1e-74;

0.9%;

Query Match Best Local Similarity

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 429)

1 (bases 1 to 429)

1 (bases 1 to 429)

1 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Tumor Gene Index

Tumor Gene Index

Tumor Gene Index

Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CONTALIBRAY Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIAN at:

www-bio.llnl.gov/bbrp/image/image.image.html
Insert Length: 1787 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 375.
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                                               ccacaggccaagaaggtcagagcccagtgaagatctgggagaccctgaactcagaaggct 26069
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/clone_lib="NCI_CGAP_CO12"
/sex="mixed"
/tissue_type="colon tumor"
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"

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         Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 691)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCM331 row: p column: 09
High quality sequence start: 4
High quality sequence stop: 615.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                         296 ATGGAGCTGTGCCGAGGCTTGGCTCCCACATAAGCACTATTATAGATGCCTCTTAGG
                                                                                                                                                            1;
                                                                                                                                Length 429;
                                                                                                                                                            1; Indels
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                  Score 245; DB 12;
Pred. No. 5.4e-72;
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/clone_TwAGES:8635576"
/clone_lib="NIH_MGC_21"
/tissue_Lype="choriocarcinoma"
/lab_host="bufl00 (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAhoI sites using the following 5' adaptor: GGGAGGAGG(S). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 439)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tational Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          891 ttttggtggagacgggcgcatgtgggcgctttgctcgctgctgcggccggacg
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100.0%; Pred. No. 4.9e-69;
tive 0; Mismatches 0;
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/clone_lib="NCI_CGAP_Pr28"
/sex="male"
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/db_xref="taxon:9606"
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High quality sequence stop: 407.
Location/Qualifiers
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unknown library type
Insert Length: 717 Std Erro
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/lab_host="DH108"
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AI201492
AI201492.1 GI:3754098
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Best Local Similarity 100.
Matches 236; Conservative
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Matches 234;
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AA522537/c
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circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (clone1Ds 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                     Length 439;
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Pred. No. 1.2e-68;
0; Mismatches 4;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:4123005"
/clone="InAGE:4123005"
/clone=Lib="NHH_MGC_17"
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/tab_host="Mull08 (phage-resistant)"
/note="Organ: muscle: Vector: poTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIX/XhoI sites using the following 5' adaptor: GGACGAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Information can be
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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DNA Sequencing by: Washington University Genome (Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/Link at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 436.
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100.0%; Pred. No. 2.1e-68;
11ve 0; Mismatches 0;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Location/Qualifiers
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AA522537
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/organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="IxAGE:979142"
/clone="IxAGE:979142"
/clone="IxAGE:979142"
/tissue_type="Lung tumor"
/lab_host="SOLR (kanamycin resistant)"
/hote="Organ: lung; Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Ollgo dT. Site_2: XhoI; Cloned unidirectionally. Primer: Ollgo dT. Bulk lung tumor. 5' adaptor sequence: 5' GAATTCGGCACGAG 3' Average insert size: 1.1 kb."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 282)

1 (bases 1 to 282)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Tangabs-rémail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmal: capabs-rémail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmart-Buck, M.D., Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone, distribution: NCI-CGAP clone distribution information can be
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Homo sapiens cDNA clone IMAGE:1552973 3',
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235 c 227 g
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om/5b03.s1 NCI_CGAP_GC4 Hc
mRNA sequence.
AA928608
AA928608.1 GI:3076899
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Best Local 3
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AA928608/c
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 433)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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qu98d07.xl NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1980109 3'
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found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 846 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 255.
Location/Qualifiers
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100.0%; Pred. No. 3.3e-66;
tive 0; Mismatches 0;
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/clone="IMAGE:1552973"
/clone_lib="NCI_CGAP_GC4"
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Proc. Natl. Acad. Sci. U.S.A.
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1 (bases 1 to 416)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagaži,M.A., Bardin,S., Costa,F.F., Nagaži,M.A., Galdman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                    ö
                                                                                                                                           /note="Organ: Stomach; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF944518 416 bp mRNA EST 22-JAN-2001
CM1-NN0211-181000-472-a12 NN0211 Homo sapiens CDNA, mRNA sequence.
BF944518
                                                                                                          /tissue_type="poorly differentiated adenocarcinoma with signet ring cell features" /lab_host="DH10B"
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Pred. No. 6.1e-66;
0; Mismatches 4;
Std Error: 0.00
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                                                          /organism="Homo sapiens"
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/clone="IMAGE:1980109"
/clone_lib="NCI_CGAP_Gas4"
           Seq primer: -400P from Gibco
High quality sequence stop: 397.
Location/Qualifiers
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/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under
                                                                                                                                                                                                                                                                                                               Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMI&t2=CMI-NN0211-
181000-472-a12&t3=2000-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 55
High quality sequence stop: 416.
Location/Qualifiers
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                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                   expressed
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                                                   Shotgun sequencing of the human transcriptome with ORF
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Soares, F., Brentani, R.R., Reis, L.F., de
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Pred. No. 3e-64;
0; Mismatches 2;
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106 c 112 g 85 t
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/clone_lib="NN0211"
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AI804749
AI804749.1 GI:5370221
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                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: DcTD/DTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRRD From University of Washingtion Genome Center. Vector

Trimming: cross_match from University of Washingtion Genome Center

PHRAP suite. Poly-T Identification: patwatch.pl from Berkeley

Drosophila Genome.washington.edu

Phtp://www.genome.washington.edu

Plate: LLCM4 row: L. column: 17

High quality sequence Stop: 225.
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                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 249)
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                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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100.0%; Pred. No. 7.7e-64;
iive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .249
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                               Unpublished (1999)
Other_ESTs: 2820640.3prime
   AW247380.1 GI:6590373
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Best Local Similarity 100.(
Matches 221; Conservative
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                                                                                                          Homo sapiens
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AI804749/c
                                                                                                      ORGANISM
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JOURNAL
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmart-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 876 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 458.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26172 gctgtgccgaggcttgggctcccacataagcactagtctatagatgcctcttaggactgg 26231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Pred. No. 1.3e-63;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2253699"
/clone_lib="NCI_CGAP_Pr28"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.8%;
                                                                                                         Tumor Gene Index
Unpublished (1997)
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177 CATTTCAAGGCAGTTTTTAAAGAAGTCATGGAAACAGACGGCGGCGCACCTTTCCTTAATC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                        AA464307 316 bp mRNA EST 10-JUN-1997 zx78c04.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 214; DB 7; Length 316;
Pred. No. 1.6e-61;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                             1. 316
/organism="Homo sapiens"
/db_xref="GDB:6039680"
/db_xref="taxon:9606"
/clone="IMAGE:809862"
/clone=lib="Soares ovary tumor NbHOT"
                                                                                                                         IMAGE:809862 5', mRNA sequence.
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AA464307.1 GI:2189191
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Best Local Similarity 99.45
Matches 314; Conservative
                                                                                                                                                                   Homo sapiens
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                                                                                                                                                            human.
                                                                                      AA464307/c
LOCUS
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ORIGIN
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JOURNAL
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                                                                                                                                 ACCESSION
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Tumor Gene Index
Unpublished (1997)

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D., cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Geneme Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW511765 316 bp mRNA EST 03-MAR-2000 xu76f03.xl NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807645 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Organ: kidney; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.2 kb. Life Technologies catalog #: 11524-014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhlni; Hominidae; Homo.
                                                                                                                                                                                             26200 agcactagtctatagatgcctcttaggactggtgcctggcacagccggggccaggagg 26259
                                                                                                atggactcacagctggggaatgtcttttgggctaactgccactctgttgttgtcctctat 14348
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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image.llnl.gov/image/html/iresources.shtml
Seq primer: -400P from Gibco
High quality sequence stop: 239.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/clone=lib="NCI_CGAP_Kid8"
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/lab_host="DH108"
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Pred. No. 1.6e-61;
0; Mismatches 1;
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Best Local Similarity 99.6
Matches 264; Conservative
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AW511765
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/tissue_type="Inbadomyosarcoma" / Lissue_type="Inbadomyosarcoma" / Lissue_type="Inbadomyosarcoma" / Lab hock="Defined profits of the post 
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NIH-WGC http://mgc.noi.nih.gov/.
  ggctgagatcctgggggaagaaggctttttgagtttgacctgaccctgcgagcagct 21345
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Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov

Tissue Procurement: ArCa
cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MG.C. Consortium/LLNL at: image.llnl.gov

Plate: LLCM999 row: e column: 03
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100.0%; Pred. No. 6.8e-61;
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/clone_lib="NIH_MGC_17"
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/db_xref='taxon:9606"
/clone_lib='Uqu014"
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/dev_stage="Adult"
/note="Organ: uterus_tumor; Vector: pucl8; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
75 a 91 c 91 g 77 t
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivelare, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-041200-365-G06&t3=2000-12-04&t4=1)
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L3-UT0114-041200-365-G06 UT0114 Homo sapiens CDNA, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                     \operatorname{Simpson}, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
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Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 1.6e-61;
0; Mismatches 2;
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BF914840.1 GI:12306298
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Matches 314; Conservative
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AUTHORS
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone_"INAGE.4564170"
/clone_lib="NIH_MGC_14"
/tissue_type="renal cell adenocarcinoma"
/lab_host="Blul08 (phage-resistant)"
/note="Organ: kidney; Vector: poTBF; Site_l: XhoI; Site_2:
EcoRI; cDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
Callfornia, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 452)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP
                                                                                                                                                       gogcaaggaccogctgoggcacctgogcacgogagagagagcggaccgtcogggtgctc 1064
                                                                                                                                                                                                                                                                                                                                BG327066 452 bp mRNA EST 27-FEB-2001
602426274F1 NIH_MGC_14 Homo sapiens CDNA clone IMAGE:4564170 5'
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1279 row: c column: 19
High quality sequence stop: 452.
Location/Qualifiers
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100.0%; Pred. No. 6.7e-61;
ive 0; Mismatches 0;
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Matches 212;
Matches 212;
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HRI human cDNA project (Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,Y., Nagai,T., Sugano,S., Isogai,T.)
                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
cggcggcccaaacaccgtgtacctgcaggtggtggcagcgggtagccgggactcgggcgc 1124
                        AU158921 535 bp mRNA EST 25-OCT-2000 AU158921 THYRO1 Homo sapiens CDNA clone THYRO1000421 3', mRNA
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
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Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1818-181-181-438-52-3951
Fax: 81-438-52-3952
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Pred. No. 6.3e-61;
0; Mismatches 4;
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/note="vector: pME185FL3"
152 c 132 g 141 t
                                                                                  cgcgctctacgtcttcccgagttcaaccggt 1156
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/db_xref="taxon:9606"
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/clone_lib="THYRO1"
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AW175582.1
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AW175582/C
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RFCIII-126L18.TV RPCI-11 Homo sapiens genomic clone RPCI-11-126L18,
DNA sequence.
AQ349651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Pleter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: T7
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Primates; Catarrhini; Hominidae; Homo.
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Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)
Other_GSSs: RPCI11-126L18.TJ
                                                               26289 tttcatttcaaggcagtttttaaagaagtcttggaaacagacggcggcacctttcctcta 26348
                                                                                                                              26349 atccagcaaagtgattccctgcacaccagagacaagcagagtaacaggatcagtgggtct 26408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
Email: hbe@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 CCAGGGGTACCTACCCTTCTGCACCTGCCTAAACTTTCTGTGGGATTCCTGCCTTCCCAG 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
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100.0%; Pred. No. 4e-60;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:7548281"
/db_xref="taxon:9606"
/clone="RRCI-11-126118"
/clone_lib="RPCI-11"
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Mammalia; Eutheria;
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Class: BAC ends.
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Best Local Similarity
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/organism="Homo sapiens"
/db_xref="taxon:9606"
//db_xref="taxon:9606"
/clone_lib="#rgr0041"
/dev_stage="Adult"
/dov_stage="Adult"
/note="forgan: Dreast; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludig.org.br
Email: sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-BF0041-030999-013-e09_1&t3=1999-09-03&t4=1)
Seq primer: puc lB forward
High quality sequence stop: 224.
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I (bases 1 to 225)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15519 aattotaggottocoagatotgtgotacactogtgaagaaaatgoacogotaggtggogo 15578
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                          90 AGTGTCCACACGATTCCATTTATTTACACCCTCCACACTCTTCAGGGGTGTCTGAAA
                                                                                                                                                                                                                                                                                                                                                                               AW175582 225 bp mRNA EST 16-NOV-19
QVO-BT0041-030999-013-e09_1 BT0041 Homo sapiens CDNA, mRNA
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159 TGGAAACAGACGCGGCACCTTTCCTCTAATCCAGCAAAGTGATTCCCTGCACACAGAG 100
                                                                                                            cagctgcaataaagattgagtttgcaa 26466
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BF477438/C
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AUTHORS
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 175.

Location/Qualifiers
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NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                         AA504146 219 bp mRNA EST 18-AUG-1997 aa59e06.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825250 3',
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Qy 13752 gcagattttggctgaagagctgtgtactcctccagatcctggtgctgcttttgtggtggt 13811
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                constructed by Bento Soares and M. Fatima Bonaldo." 46~\mathrm{c} 43 g 82~\mathrm{t}
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/db_xref="taxon:9606"
/clone="InAGE:82520"
/clone_lib="NCI_CGAP_GCBI"
/tissue_type="germinal center B cell"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%; Score 207; DB 8; 1100.0%; Pred. No. 4.1e-59; ive 0; Mismatches 0;
                                                              Qy 13812 agaatgtccagatgaaagcttcattcaac 13840
                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                               AGAATGTCCAGATGAAAGCTTCATTCAAC 1
                                                                                                                                                                                                                                      AA504146.1 GI:2240306
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3438945"
/clone="IMAGE:3488945"
/clone="IMAGE:348945"
/clone="IMAGE:47899606"
/ilssue_type="glioblastoma (pooled)"
/ilssue_type="gliobl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, Ph.D. crayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
BF477438 409 bp mRNA EST 05-DEC-2000
nac60h05.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3438945
3', mRNA sequence.
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Pred. No. 1.6e-58;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Best Local Similarity 99.0
Matches 405; Conservative
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452 CAGGCCAAGAAGGTCAGAGCCCCAGTGAAGATCTGGGAGACCCTGAACTCAGAAGGCTGTG 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 541)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

RESEARTCH INSTITUTE; CDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.
                           26356 aaagtgattccctgcacaccagagacaagcagagtaacaggatcagtgggtctaagtgtc 26415
349 GGTAGAAGCTGAAGAGCACGGTCCCCCAGGAGGCAGCTCAGGATAGGTGTATGGAGCTG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                           AU148489 541 bp mRNA EST 25-OCT-2000 AU148489 NT2RM4 Homo sapiens cDNA clone NT2RM4000375 3', mRNA
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                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Takao 180gai
Contact: Takao 180gai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
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Pred. No. 3.1e-58;
0; Mismatches 2;
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/clone_lib="NT2RM4"
/cell_type="teratocarcinoma"
/cell_line="NT2"
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/db_xref="taxon:9606"
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Enail: wobert strausberg, Ph.D.

Enail: Gapbs-Fremail.ih.gov

This clone is available royalty-free through LLNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 71 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 233.

Location/Qualifiers

1. .416

Adb xref="theory sequence" 133.

Adb xref="theory sequence" 134.

Alone="IMAGE:1689849"

Alone="IMAGE:1689849"

Alone="IMAGE:1689849"

Alone="IMAGE:1689849"

Alone="Theory sequence theory sequenc
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qa46h05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1689849
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 416)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                    26192
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Pred. No. 3.5e-56;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI141263.1 GI:3648720
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//note="Vector: lambda pSB; Site_1: BamHI; Site_2: ECORI; First strand cDNA was primed with an anchored Anol-oilgo(dT) primer [5'GGAGGACTGAGGGGCGCGCGGGGGGGG(T)VN 3''; V=A,C,G,G,N=A,C,G,T] and then dG tailed. Second strand was primed with a BamH1-dC primer [5'AGAGGCTGGATCGGGCCGCAATAATAAATAATAAT(C) 3']. Bouble-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: clones@txccc.org
Seq primer: M13 primer.
Location/Qualifiers
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    186
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BE243887
BE243887.1 GI:9095627
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                                                                                                                                                                                                                                                                                                                                                                                                                                          388 AGCGGGCCCACACAGAGG 371
    O
                                                                                                                       Matches 198; Conservative
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                                                                                                    Similarity
      ಹ
  124
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Best Local 3
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Adev_State="Addit"

Note="Organ: head_neck; Vector: puc18; Site_1: Smal;

Site_2: Smal; A min1-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and CDNA amplification were performed under

low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1-RC1&t2-RC1-HT0217-
201199-022-h08&t3-1999-11-20&t4-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW378247 650 bp mRNA EST 04-FEB-2000
RC1-HT0217-201199-022-h08 HT0217 Homo sapiens cDNA, mRNA sequence.
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I (bases 1 to 650)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Fig. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                     ccctgcacaccagagacaagcagagtaacaggatcagtgggtctaagtgtccgagactta 26424
                                                                                                                                                                                                                                                                               26245 cgcgggccaggaggctgccacacggaagcaagcagatgaactaatttcatttcaaggcag 26304
                                                                                                                                                                                                                                                                                                                                                               tttttaaagaagtcttggaaacagacggcggcacctttcctctaatccagcaaagtgatt 26364
                                                                                                                                                                                                                                                                                                    236 TGCGGGCCAGGAGGCTGCCACCACGGAAGCAAGCAAGATGAACTAATTTCATTTCAAGGCAG 177
                                                                                                                                                                                                                                        296 TTGGGGTCCCACATAAGCACTAGTCTATAGATGCCTCTTAGGACTGGTGCCTGGCACAGC 237
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4; Indels
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/db_xref="taxon:9606"
/clone_lib="HT0217"
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High quality sequence stop: 74.
Location/Qualifiers
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Matches 398; Conservative
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1 (bases 1 to 414)
Well,Y. Tsang,Y.F.N., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D.
Bouck,J., Gibbs,R.A. and Margolin,J.F.
Pediatric Leukemia cDNA Sequencing Project
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Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                      BE243887 414 bp mRNA EST 15-NOV-2000 TCBAPIE1522 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAPI522, mRNA
                                                                                                                                                                                                   25810 aggtctgctttggagactttccaacaatgcccaagctgattcccccactgaaagccctgt 25869
                                                                                                                                                                                                                                                                                                        25870 ttgctggcgacatcgaggagatggaggagcgcagggagaaagcgggaagctgcggcaggtgc 25929
                                                                                                                                                                                                                              /organism="Homo sapiens"
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/clone=lib="Pediatric pre-B cell acute lymphoblastic |
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                                                                                             Length 650;
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                                                                                             0.7%; Score 198; DB 115;
100.0%; Pred. No. 3e-56;
ative 0; Mismatches 0;
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/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
148
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Gaps

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/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="InAGE:4585858"
/clone=lib="NHHE,MGC:44"
/tissue_type="renal cell adenocarcinoma"
/tlab_host="NHHIB0 (phage-resistant)"
/note="Organ: kidney; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1:8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E. (Dabases 1 to 860)
L. Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1312 row: p column: 02
High quality sequence stop: 705.
tissue mRNA and cDNA amplification were performed under low stringency conditions." 169~c~149~q~135~t
                                                                                                                                                                                                                                                                                                       BG422177 860 bp mRNA EST 14-MAR-2001
602446808F1 NIH_MGC_14 Homo sapiens CDNA clone IMAGE:4585585 5',
mRNA sequence.
                                                                                                                                                                                                                                                          387 CGGCCCCACACAGAGCCACAGGCCAAAGAAGGTCAGAGCCCAGTGAAGATCTGGGAGA 328
                                                                                                                                                                                                                     25992 egggeecacacagaggagecacaggeeaagaaggteagageecagtgaagatetgggaga
                                                                                                                                   Length 552;
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                                                                                                                               0.7%; Score 193; DB 147;
100.0%; Pred. No. 1.5e-54;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 193; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 552)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-HT0217-131199-021-g10&t3=1999-11-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF349810 552 bp mRNA EST 22-NOV-2000
CL-HT0217-131199-021-g10 HT0217 Homo sapiens CDNA, mRNA sequence.
BF349810.1 GI:11308884
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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0
                                                                                                             Length 414;
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                                                                                                                                                      Indels
                                                                                                        0.7%; Score 195; DB 165;
100.0%; Pred. No. 3.6e-55;
Live 0; Mismatches 0;
                      74
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/db_xref="taxon:9606"
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                      143
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Best Local Similarity 100.(
Matches 195; Conservative
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61 GCGCAGGCACCCGCCCGCCGCGGAGCGGCCGCGAAGGACCCGCTGCGGCACCTGCGCACG 120
human.
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/tissue_type="Thabdomyosarcoma"
/ibb_host="NIH_MGC_17"
/ibb_host="NIH_MGC_17"
/note="Organ: muscle; Vector: poTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAGGG). Size-selected 500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZaP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
81 a 124 c 132 g 79 t
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                  25949 ggagctggcaggcggcctggaggatggggagcctcagcagaagcgggcccacacagagga 26008
                                                                                                                                                                         gccacaggccaagaaggtcagagcccagtgaagatctgggagaccctgaactcagaaggc 26068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCNBS row: f column: 12
High quality sequence stop: 416.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE298273 416 bp mRNA EST 20-JUL-2000 601118143F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3027851 5'
                                                                                                                               387 GGAGCTGGCAGGCGTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 416)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                           447 GCCACAGGCCAAGAAGGTCAGAGCCCCAGTGAAGATCTGGGAGACCCTGAAACTCAGAAGGC
                    Length 860;
                                                        Indels
                0.7%; Score 193; DB 153;
100.0%; Pred. No. 1.3e-54;
tive 0; Mismatches 0;
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Pred. No. 1.7e-53;
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/db_xref="taxon:9606"
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Best Local Similarity 99.6%;
Matches 240; Conservative
                                                    Conservative
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                                                    193;
                Query Match
Best Local S:
Matches 193
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 424)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@warson.wustl.edu
Insert Size: 1152
Insert Size: 1152
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1152 Std Error: 0.00
Seq primer: Promega - 21m13
High quality sequence stop: 315.
    20-JUN-1995
03318 424 bp mRNA EST 20-JUN-
147e10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                           Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                         MAGE:151914 3', mRNA sequence.
                                                                                H03318.1 GI:866251
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0; Mismatches

277

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3876223"
/clone_lib="NHL WGC_68"
/tissue_type="large realstant)"
/lab_host="DHIOB (phage-realstant)"
/note="Organ: lung: Vector: pCMV-SPORT6; Site_1: Not1:
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.

Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.

National to 577)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

CONTACT: 
                                                                                                                                                                                      26102 ctgccctccttgctggtagaagctgaagagcacggtcccccaggaggcagctcaggatag 26161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM9636 row: k column: 08
High quality sequence stop: 577.
Location/Qualifiers
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                                               Gaps
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Pred. No. 7.8e-50;
0; Mismatches 0;
                      red. No. 3.8e-50;
Mismatches 0;
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                      Pred. No.
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100.0%; PIC
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                    Best Local Similarity 100.
Matches 180; Conservative
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NCI-GAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                26270 aagcaagcagatgaactaatttcatttcaaggcagtttttaaagaagtcttggaaacaga 26329
                                                                                                                                                                                                                                                                                ox02d12.s1 Soares_fetal_liver.spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:1655159 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
INSERT Length: 749 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 455.
Location/Qualifiers
                                                                                                                                                                                                                                      195 AAGCAAGCAGATGAACTAATTTCAATGCCAGTTTTTAAAGAAGTCTTGGAAACAGA 136
                                                                                                                                            Gaps
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0
                                                                                            Length 424;
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                                                                                                                                            Indels
                                                                                       0.7%; Score 182; DB 157;
100.0%; Pred. No. 8.5e-51;
iive 0; Mismatches 0;
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Unpublished (1997)
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Www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 663 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 366.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Banall: gapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                      Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 398)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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110 AGTGATTCCCTGCACACCAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .398
//organism="Homo sapiens"
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/clone="IMAGE:1589387"
/clone="lb="NoI_cGAP_Kid5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 178; DB 14;
Pred. No. 1.9e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                       AA948352.1 GI:3109605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.78;
                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 228; Conservative
                                                                                                                                                                                                                                                                                                            Tumor Gene Index
                                                                                                                     mRNA sequence.
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                                                                                                                                       AA94835
                                                                                                                                                                                         human.
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Best Local 3
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                                                                AA948352/c
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TITLE
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/clone="INAGE:108533"
/clone_lib="NCI_CGAP_GC5"
/tissue_type="germ cell tumor"
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a 101 c 90 g 135 t
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information can be
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                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 406)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA583412 406 bp mRNA EST 08-SEP-1997 nn42b10.s1 NCI_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086523 3',
                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26090 acgcacccgtatctgccctccttgctggtagaagctgaagagcacggtcccccaggaggc 26149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26210 tatagatgcctcttaggactggtgcctggcacagccgcgggccagaggaggctgccacacgg 26269
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 ACGCACCCGTATCTGCCCTCCTTGCTGGTAGAAGCTGAAGAGCACGGTCCCCCAGGAGGC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 CGGCGCCACCTTTCCTCTAATCCAGCAAAATGATTCCCTGCACACCAGGACAAGCAGAG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 173; DB 9;
98.9%; Pred. No. 9.2e-48;
tive 0; Mismatches 4,
                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                              AA583412.1 GI:2368021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 373; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .406
                                                       mRNA sequence.
AA583412
                                                                                                                                                                                             Homo sapiens
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42 ACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTGCAA 1
                                                                                                                       mRNA sequence.
                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 171; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71
                                                                                                                                         AA766184
                                                                                                                                                                                            human.
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                                                                                   LOCUS
                                                                    AA766184/c
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                                                                                                                                                                                                                                                                              AUTHORS
TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anote—"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 68263-687239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26245 cgcgggccaggaggctgccacacggaagcaagcagatgaactaatttcatttcaaggcag 26304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 865 Extern: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 213.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 CGCGGGCCAGGAGGCTGCCACACGGAAGCAAGCAGGATGAACTAATTTCATTTCAAGGCAG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
106 TAACAGGATCAGTGGGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAAT 47
                                                                                                                                                                        19-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
,
                                                                                                                                                                       AA905284 222 bp mRNA EST 19-MA oj96b07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1506133 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .222
/organism="Homo sapiens"
/organism="taxon:9606"
/clone="IMAGE:1506133"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 171; DB 13;
Pred. No. 5.3e-47;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 g
                                                                                                                                                                                                                                        AA905284.1 GI:3040407
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                                                 26450 aaagattgagtttgcaa 26466
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                                                                                 46 AAAGATTGAGTTTGCAA 30
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                                                                                                                                                                                                                                                                                human.
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                                                                                                                                    RESULT 79
AA905284/c
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KEYWORDS
SOURCE
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1. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
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0
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information can be
AA766184 318 bp mRNA EST 08-FEB-1998 oa12f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304777 3',
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 318)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Ph.D., Gerald Marti, M.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 318;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.B. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 171; DB 11;
100.0%; Pred. No. 4.7e-47;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www.bio.lnl.gov/bbrpy/image/image.html
Insert Length: 1277 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 288.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:130477"
                                                                                          AA766184.1 GI:2817422
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                                                                                                                                                                                                                                                                                                   Tumor Gene Index
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DEFINITION AA954438/c

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ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

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EUKaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 447)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore
Schellenberg, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E.,
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26086 acgcacgcacccgtatctgccctccttgctggtagaagctgaagagcacggtcccccagg 26145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 727 Std Error: 0.00
Seg primer: mob.REGAFET
High quality sequence stop: 409.
Location/Qualifiers
  W86158 447 bp mRNA EST 02-FEB-1997 2159009.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens CDNA clone IMAGE:416368 3', mRNA sequence.
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/organism="Homo sapiens"
/db_xref="GDB:1324838"
/db_xref="taxon:19606"
/clone="ImAGE:416368"
/clone="InAGE:416368"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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100.0%; Pred. No. 9.4e-45;
tive 0; Mismatches 0; Indels 0;
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Best Local Similarity 100.0
Matches 164; Conservative
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                                                                                                                                                                               Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 220)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Emal: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 837 Std Error: 0.00
Seq primer: -40ml3 fwd. Ef from Amersham
High quality sequence stop: 167.
Location/Qualifiers
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                                                                                                                        AA954438 220 bp mRNA EST 07-JUL-1998 on85e06.sl Soares_NFL_T_GBC_Sl Homo sapiens cDNA clone IMAGE:1563490 3', mRNA sequence.
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198 GCAGATGAACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAAC 148
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/db_xref="taxon:9606"
/clone="IMAGE:1563490"
/clone_lib="Soares_NFL_T_GBC_S1"
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                                    26467 ttgtga 26472
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                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be
found through the I.M.G.E. Consortium/LLNL at:
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                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 372)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                  tn94b10.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2177179 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/clone_lib="NCI_CGAP_Ut2"
/clssue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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Pred. No. 4.7e-44;
0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                     www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 737 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 342.
Location/Qualifiers
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Best Local Similarity 98.9
Matches 362; Conservative
                                                                       mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 374)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. (Uppublished (1997)
                                                                                                                                                                                                                          RNA 12-MAR-1998 neuronal precursor 937230 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 3011 Std Error: 0.00
Seq primer: -41n13 fwd. Er from Amersham.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1e-43;
0; Mismatches 4; Indels
                                                                                                                                                                                                                    AA223338 374 bp mRNA ES7
zr05h05.s1 Stratagene NT2 neuronal precursc
cDNA clone IMAGE:650649 3', mRNA sequence.
AA223338.1 GI:1843862
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/db_xref="GDB:5277238"
/db_xref="taxon:9606"
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Best Local Similarity 98.9%;
Matches 361; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI468143 421 bp mRNA EST 30-MAR-1999 tf92g05.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2106776 3' similar to SW:YK59_YEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2_MTD1 INTERGENIC REGION.;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Bickaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 421)
1 (bases 2 to 421)
1 (bases 2 to 421)
1 (bases 3 to 421)
1 (bases 3 to 421)
1 (bases 4 to 421)
1 (bases 4 to 421)
1 (bases 4 to 421)
1 (bases 5 to 421)
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1 (bases 7 to 421)
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                                                                                            26401
                                                                                                                                                                                                              26402 tgggtctaagtgtccgagacttaacgaaaatagtatttcagctgcaataaagattgagtt 26461
74 TGGGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTT 15
                                                                                            tcctctaatccagcaaagtgattccctgcacaccagagacaagcagagtaacaggatcag
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100.0%; Pred. No. 1e-42;
Live 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 733 Std Error: 0.00
Seg primer: -40UP from Gibco.
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Matches 158; Conservative
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/organism="Homo sapiens"
/do_raref="texan:9606"
/clone="lib="Soares_fetal_lung_NDHL19w"
/dev_stage="19 weeks"
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/dev_stage="10
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AI200296 451 bp mRNA EST 14-OCT-1998
R$6512.X Soares_fetal_lung_NbHLI9W HOMO sapiens cDNA clone
IMAGE:1756895 3' similar to SW:YK59, YEAST P36159 HYPOTHETICAL 96.8
KD PROTEIN IN SIS2-WIDI INTERGENIC REGION.; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 451)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco
High quality sequence stop: 442.
Location/Qualifiers
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100.0%; Pred. No. 9.8e-43;
tive 0; Mismatches 0;
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AI200296.1 GI:3752902
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Matches 158; Conservative
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Gaps

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polylinker; Site_l: Not I: Site_2: Eco RI; NCI_CGAP_Sub6
is a subtracted library derived from BW, which consists of
a mixture of four normalized libraries: NCI_CGAP_Brn50,
NCI_CGAP_Lul3, NCI_CGAP_Ov18, GBC1: The NCI_CGAP_Brn50,
NCI_CGAP_Lul3 NCI_CGAP_Ov18, GBC1: The NCI_CGAP_Brn50,
preparation of BW was used as a tracer in a subtractive
hybridization with a driver comprising: the IMAGE pool
lybridization with a driver comprising: the IMAGE pool
lybridization with a driver comprising: the IMAGE pool
licam 3338-3342, 3322-3725, 3376-123391,
1456008-1456775,1500552-1502855), NCI_CGAP_Lul5 pool licam 334-337, 3681-3867,
1323912-1325831, 1471368-1472903, 1492104-1493255);
NCI_CGAP_Lul5 pool licam 3776-3720, 3733-3735 (IMAGE
CloneIDS 1257096-1256631,1469064-1470983, 1475592-1476743
); NCI_CGAP_Lul5 pool licam 2457-2459, 2758-2759,
121728-1220615; NCI_CGAP_COLD pool licam 240-2653,
121728-1220615; NCI_CGAP_COLD pool licam 2 pool of 3,840
arrayed clones from NCI_CGAP_Sub1 (IMAGE CloneIDS
2710546-2712455)

cool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE CloneIDS
2710546-2712455)

cool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE CloneIDS
2710545-2712455)

cool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE CloneIDS
2710546-2712455)

cool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE CloneIDS
2710546-2712455)

cool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE CloneIDS
2710546-2712455)

cool of the driver population), plus a pool of the driver population), plus a pool of the driver population), plus a pool of the driver population was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery. Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
POLYA-NO.
                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 228)
NCI-CGAP http://www.ncbi.nhm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           AW296524 228 bp mRNA EST 16-JAN-2000 UI-H-BW0-aiv-a-09-0-UI.sl NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730521 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/clone="IMAGE:2730521"
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TAG_LIB=NCI_CGAP-Lul3
TAG_TISSUE=lung
TAG_SEO=GCCGG"
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                                                                                                                                                    AW296524.1 GI:6703160
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Unpublished (1997)
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Best Local Similarity 100.
Matches 157; Conservative
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Contract: Kober: Strausberg, Ph.D.

Email: cgapbs-r@mail.ih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmeart: Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento

Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

Clone distribution: NCI-CGAP Clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:

Info@image.llnl.gov

High quality sequence stop: 491.

Location/Ouallifers

1. 526

/ Organism="Homo sapiess"

/ Action="InAGE: 356586"

/ Clone="InAGE: 35658
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1 (bases 1 to 526)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Optublished (1997)
                                                                                                                                                                                                                                                                                       7n68a10.xl NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:356986 3's milar to TR:Q9V5J4 Q9V5J4 CG3298 PROTEIN. ;, mRNA sequence. BF196304.1 GI:11084107
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100.0%; Pred. No. 9.3e-43;
live 0; Mismatches 0; Indels 0;
Contact: Robert Strausberg, Ph.D.
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Best Local Similarity 100.0
Matches 158; Conservative
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AW296524
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FEATURES

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 Length 228;
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0.6%; Score 157; DB 114;
100.0%; Pred. No. 2.7e-42;
tive 0; Mismatches 0;
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Query Match
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/clone_lib="wnN0045"
/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: puc18; Site_l: SmaI;
Site_2: SmaI; A min1-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.

74 g 77 g
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1 (bases 1 to 317)

1 bias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Sinpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=QV2&t2=QV2-NN0045-
121200-545-g10&t3=2000-12-12&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 317.
                                                                                                                                                                                                                                                                                     BF961941 317 bp mRNA EST 22-JAN-2001

VQZ-NNO045-121200-545-g10 NN0045 Homo sapiens CDNA, mRNA sequence.

BF961941.1 GI:12379216
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
                                                                         9
1000 cggccgcgcaaggacccgctgcggcacctgcgcacgcgagagaagcgcggaccgtcgggg
                     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Pred. No. 2.4e-42;
0; Mismatches 0;
                                                                                                                                                    1120 ggcgccgcgctctacgtcttctccgagttcaaccggt 1156
                                                                                                                                                                        121 GGCGCCGCCTCTACGTCTTCTCCCGAGTTCAACCGGT 157
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/clone="Index: Jaxon: 3000"
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/note="Vector: pT713-Pac; Site_1: NotI; Site_2: Eco RI;
/note: pT713-Pac; Site_1: Not
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Oligo-dr track not found, Not I site shown in beginning of sequising likely internal to the message. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1000 eggecgegaaaggaccegetgeggeacetgegeaegegagaagagegeggacegtegggg 1059
1 (bases 1 to 493)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW575677 493 bp mRNA EST 15-MAR-2000 UI-HF-BM0-ad1-b-07-0-UI.s1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3061957 3', mRNA sequence.
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Seg primer: M13 Forward
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100.0%; Pred. No. 2.1e-42;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                          ggcgccgcgctctacgtcttctccgagttcaaccggt 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/note="Organ: lung_tumor; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                    1 (bases I to 354)
Dias Neto,E., Garcia,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
.M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMO&t2=CMO-ET0124-021100-676-e02&t3=2000-11-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence start: 5
High quality sequence stop: 354.
   CM0-ET0124-021100-676-e02 ET0124 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                       Homo sapiens
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 354)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 ACTCCTTTTTCCCCCAGAAGGTAATGTCTTAGCACCGGGGCTTCTCTCTGCAAAATGGGT 235
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20202663
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100.0%; Pred. No. 5e-42;
live 0; Mismatches 0;
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                                                             GI:12263061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: +55-11-2704922
Fax: +55-11-2707001
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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL, send email to: infoélmage.lln.jgvv

Seq primer: -40UP from Gloco

High quality sequence stop: 507.

Location/Qualifiers

1. 553

//Oganism="Homo sapiens"
// Ab_xref="taxon:5606"
// Clone="IMAGE:3644670"
// Clone="IMAGE:3644670"
// Clone="IMAGE:3644670"
// Lissue_type="fibrotheoma"
// Listue_type="fibrotheoma"
/
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 553)

8 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

1. Contact: Robert Strausberg, Ph.D.
Email: cgapbs.remail.nih.gov.
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                              BF434169 553 bp mRNA EST 29-NOV-2000 7099f04.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3644670 similar to TR:Q9V5J4 Q9V5J4 CG3298 PROTEIN. ;, mRNA sequence. BF434169.1 GI:11446441
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100.0%; Pred. No. 2e-42;
Live 0; Mismatches 0; Indels 0
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/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: Sfi1 (ggccgctcggcc); Site_2: Sfi1 (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATATGGCC3' and 3' adaptor sequence: 5'-ATTATAGAGCGAGGCGCGCAAGG-dT (30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb): 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM766 row: p column: 12

High quality sequence stop: 611.

Location/Qualifiers

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                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I thases 1 to 726)
11 HGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Pred. No. 8.5e-42;
0; Mismatches 0; Indels 1
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_60"
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                  BF102508.1 GI:10885034
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RESULT 9 BE883616

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1..370
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:399527"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="BHI0B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
94 a 100 c 106 g 70 t
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 370)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

4 National Institutes of Health, Mammalian Gene Collection (MGC)

5 Ontact: Robert Strausberg, Ph.D.

6 Contact: Robert Strausberg, Ph.D.

7 Email: cgapbs-rémail.nih.gov

7 Tissue Procurement: ATCC

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9723 row; f column: 24

High quality sequence stop: 370.

Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                               'n
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A EST 20-OCT-2000 sapiens cDNA clone IMAGE:3909527 !
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/clone="Indexions" (clone="Indexions") /clone="Indexions" (clone="Indexions") /clone="Indexions" (clone="Indexions") /clone="Indexions" (clone="Indexions") /close="Organ: Kidney: Vector: pOTB7; Site_1: XhoI; Site_2: Anote="Organ: Kidney: Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/lab_host="DH10B (phage-resistant)"
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                                               1. 754
/organism="Homo sapiens"
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/clone_lib="NIH_MGC_21"
  High quality sequence stop: 714.
                                                                                            /db_xref="taxon:9606"
                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.69
Best Local Similarity 100.1
Matches 152; Conservative
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BG336190
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                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="inba"NIH_MGC_9"
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/note="Organ: ovary: Vector: poTB7: Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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E 1 (bases 1 to 754)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Onpublished (1999)

L Onpublished (1999)

Email: cgapba-remail..nih.gov
Tissue Procurement: DCTD/DTP
CONT ibrary Preparation: Ling Hong/Rubin Laboratory
CONA ibrary Preparation: Ling Hong/Rubin Laboratory
CONA ibrary Arrayed by: The I.M.A.G.E. Consortium (LML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://mage.llnl.gov
Plate; LLCM1271 row: k column: 21
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                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Glone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM518 row: a column: 03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 CAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATTATGCT 358
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              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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100.0%; Pred. No. 4.1e-41;
ative 0; Mismatches 0;
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                                                                                                                                                                                                            High quality sequence stop: 672.
Location/Qualifiers
1. 677
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BG324135
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Matches 153;
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ORIGIN
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BG324135
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Contact: Robert Strausberg, Ph.D.
Email: capabs-rémail.nih.gov
Tissue Procurement: Arcc
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1222 row: p column: 19
High quality Sequence stop: 610.
Location/Qualifiers
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG336190 906 bp mRNA EST 27-FEB-2001 602404980F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4542594 5', mRNA sequence.
                                                                                                                                                                                                                                            981 ggcacccgcccgccgcgagcggccgcgaaggacccgctgcggcacctgcgcacgcgaga 1040
                                                                                                                          921 ttgetegetgetgeggteegggeeggaegeaceatgtegeagggaegeaceatategea 980
                                                                                                                                                      0; Gaps
   Length 754;
                                                                Indels
0.6%; Score 152; DB 152;
100.0%; Pred. No. 8.6e-41;
tive 0; Mismatches 0;
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/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into BCORI/AhoI sites using the following 5' adaptor: GGGAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Kit (Strategene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 157)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=0V2&t2=0V2-NN0045-051200-517-h06&t3=2000-12-05&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 157.

Location/Qualifiers
1. 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF960051 157 bp mRNA EST 22-JAN-2001
QV2-NN0045-051200-517-h06 NN0045 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                   Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                        ;
0
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O.6%; Score 152; DB 152; Length 906;
Best Local Similarity 100.0%; Pred. No. 8.1e-41;
Matches 152; Conservative 0; Mismatches 0; Indels 0
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20202663
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/db_xref="taxon:9606"
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BF960051/c
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/ Organism "Homo sapiens"
//db_xref "taxon:9606"
//db_xref "taxon:9606"
//clone_lib="NCI_CGAP_Pr23"
//clone_lib="NCI_CGAP_Pr23"
//sex "male, pooled"
//tissue_type="prostate tumor"
//lab_host="SOLR (kanamycin resistant)"
//lab_host="SOLR (kanamycin center incorrection in the control of the contro
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information can be
derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 390)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6140 taaagacattcatgtctggttttacttacatgtgaagagagtaccaagcagtaggggtat 6199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6080 cagggccagatgatgtggtcttagcttaggaaaagagttagtcttgtccttgaacttggc 6139
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequen
Clone distribution: NCI-CGAP clone distribution inform
                                                                                                                                                                                                                                                                                                                                             Length 157;
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www.bio.llnl.gov/bbrp/image/image.html
Seg primer: 4-0ml3 fwd. ET from Amersham
High quality sequence stop: 378.
Location/Qualifiers
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100.0%; Pred. No. 7.3e-38;
ive 0; Mismatches 0;
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 144; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Li (bases I to 278)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=IL0-ST0002-160
Seq_primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
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cctgccccagaatacgaggatgaaaccatgacagtttaccagatc cttatgcctaatgatagtgattatgctttggaatattagatac ctgactgaaggcagaaggcagcagggaggaggaggaggaatgtgccgga ctgactgaaggcagaaggcagcaggaaggaaggaatgtgccgga 1tgattacagcaacctaaaagaagtgttgttgggggttagaagct gctcagatgccttctctacctgaccctgctgtagccacccca

| Oy 7561 gacagtcaaat | Qy 7621 gagttaaaagt | 7681 ccttaaca 7681 ccttaaca | 7741 gtctagt 7741 gtctagt | 7801 aaagact 7801 aaagact | /8bl atatgtgtt 7861 atatgtgttt | /921 atgtgtcat: 7921 atgtgtcat: | 7981 gttttto 7981 gtttto | 8041 attagtg | 8101 aatta 8101 aatta | 8161 gataato | 8221 ctggtcgt | 8281 ggtcttggtc 8281 ggtcttggtc | 8341 ttacctgaga | 8401 tggctcacgc | 8461 gagtttgagaa | 521 tago 521 tago | Qy 8581 atcgcttgaac |
|---|--|--|--|---|--|--|---|-------------------------------------|--|---|--|--|---|----------------------|--------------------------|---|--|
| acccca 6480 Lccatgg 6540 | tccatgg 6540 agttttg 6600 adttttg 6600 | 0999 | itta 6720 ta 6720 | tag 6780 tag 6780 | cacgtt 6840 cacgtt 6840 | itaggac 6900 taggac 6900 | tactgtatag 6960 tactgtatag 6960 | 7020 | ygtgaac 7080 gtgaac 7080 | tcagtc 7140 tcagtc 7140 | gtaata 7200 gtaata 7200 | aatg 7260 1 aatg 7260 | 39c 7320 19c 7320 | ygcagcctgca 7380 | tg 7440 tg 7440 | oat 7500 oat 7500 | 7560 |
| ggottgotcctcctgctcagatgccttctctcacctgaccctgctgtagccctgattttcagccctgttcttcgccctgatttcagcaccctgttttttgt | jagttgcatccacctgtttgttgtccatttccagcaccctgttcttc cgacagttaactttcatatgtgatttgcgtgatcgatgttaacatgc | Cactgittitteagtgiccagageceteagtgaettacgi | agcgaattttt agcgaattttt | actaaatgtaaaatgaggctccttcttgagataggtaccctttgggtctatgtgt | ttagatë ttagatë | gttgagttggtactgtggccgaggctgtgagctaagcagaaacataaacatta: | ataggtgcagcccagaaaccaggtaggaagttaactaact | attggcgttctggcattcccatgtatgaac; | ggctgtcagctcaccttgtgcagtgtgtaatttggtggtatctgtactgaccag | agaggagggaaagcaccaaccatggcagagtccagaaaggcctctcagcaggc | gogatottcagactccgagtygaatgaaaatgagccacaccttccaca | gtataaacaaaacagagcagcagaaaggcttgcgttttcttaattctctgccttgt | cttgtagagagtcattattgtaagaaagccaggtgtgtaaacagatccttcttctg; | ggttgttgtaaaggtg | cagggtctgggtagg | tgttctgttttcccagaggagaacaggcctgacaaacggattcattttgtatttt | taatgtaacatttatgcaaattttccattaatgtggaaactataactgctaagccaatga |
| 6421 | 6541 6541 6541 | | 6661 | 6721 | 6781 6781 | 6841 | 6901 | 6961 | 7021 | 7081 | 7141 | 7201 | 7261 | 7321 | 7381 | 7441 | 7501 |
| Db Qy | g & g | Qy | Qy Db | Oy Db | Qy | Oy Op | Qy | Qy | Qy Db | Qy Db | Qy Db | Oy Dp | Qy Db | Oy Op | Qy Dp | Qy Db | oy ob |

| δŏ | 7561 | gacagtcaaatcagtgagaggctctgcacgtcttccagaatgacagcccactgggaaacg | 62 |
|----|------|---|------|
| മ് | ۰ | acagicaaaicagigagaggeicigcacgicticcagaaigacagcccacigggaaac | 9 |
| οy | 7621 | | |
| ф | 7621 | agttaaaagtccaagatgagatgtagctcaggagtcaggcgcttcgggagtttgttg | |
| ΟY | 7681 | acagaaggtcagcgttggcaaagctcggcagctccttttctgtcctgaggt | 7740 |
| qq | 7681 | cttaacagaaggtcagcgttggcaaagctcggcagctcctcttctgtcctgaggtct | 7740 |
| Οy | 7741 | tctagtgactgagaacaggctgacccctatgtgctgtccttgtttggatggcaccg | 7800 |
| q | ~* | ctgagaacaggctgacccctatgtgtgtgtcttgtttggatggcaccggg | œ |
| δλ | 7801 | aagactgacaccagcatttctctgcaggcctttgaacttttgtgttatttcatata | 7860 |
| q | 7801 | | ω |
| Qy | 7861 | tatgtgttataaagcacattacaatatatttttctctgtcttctccagtcctaggtga | 6 |
| qq | 7861 | | 92 |
| δy | | tgtgtcatttaaaaaaaatttcacttgccattctaaagtttttctggtgagagttt | 7980 |
| Op | | | 7980 |
| Qy | 7981 | tttttcatttacgcaaacacatctccacataagtagggaaaaaagtcttcttg | 8040 |
| qq | | ttttatttatgaaacacatctccacataagtaggaaaaaagtctttttgagta | 8040 |
| ΟŊ | 4 | tagtgtcttcagcctttgtattgggacagtagcgtccattaatttttatgtgaagt | 8100 |
| qq | 8041 | ttagtgtcttcagcctttgtattgggacagtagcgtccattaattttatgtgaagtg | 8100 |
| Qy | 8101 | ttaggtatcgggtcataatcagtctgtgatgtcttcacagctttcacatttacct | 8160 |
| qq | | attaggtatcgggtcataatcagtctgtgatgtcttcacagctttcacatttaccttg | 8160 |
| Qy | 8161 | tgtgtttttcctcaggtgttagccagagaagaggggtcagggactct | 8220 |
| qq | 8161 | ataatcaagtgtgtttttcctcaggtgttagccagagaagaggggtcagggactcttc | 8220 |
| Οy | 8221 | ggtcgtagctttcatctgtaaggtaaggtaagactttccggagggctgtacatgactg | 8280 |
| qa | 8221 | tggtcgtagctttcatctgtaaggtaaggtaagactttccggagggctgtacatgac | 8280 |
| Qy | 8281 | gtcttggtcagcgacctctggtttgcactttttcattaatttgagggtaggca | 8340 |
| QQ | 8281 | tettggtcagcgacctctggtttgcactttttcattaatttgagggtaggcactcc | 8340 |
| Qy | 8341 | tacctgagacaagaagagatagcagatcttcagaaaagctgatggaaggccggggtgca | 8400 |
| qq | 8341 | tacctgagacaagaagagatagcagatcttcagaaaagctgatggaagg | 4 |
| ογ | 0 | ggctcacgcctgtaatcccagcactttgggagtccaaggcaggtggatcacgaggtca | 8460 |
| qa | 8401 | incerial (1119) 1119 1199 | 8460 |
| Qy | | agtttgagaacagcctgaccaacgtggtgaaaccctgtctgt | 8520 |
| QQ | 8461 | gtttgagaacagcctgaccaacgtggtgaaaccctgtctgt | 8520 |
| δλ | 2 | tgggtgtggtggcgcatgcctgtaatcccagctacttgagaggccaaggcaa | 8580 |
| QQ | | agetgggtgtggtggcgcatgcctgtaatcccagctacttgagaggccaaggcaagag | 8580 |
| δλ | 8581 | cttgaacacaggaggcggaggttgcagtgagttgagattgcaccattgcactcc | 8640 |
| qq | 8581 | tegettgaacacaggaggeggaggttgcagtgagttgagattgcaccattgcactcca | 8640 |

| 9721 | 9781 | 9781 | 9841 t | 9841 t | 9901 t | 9901 | 9961 | 9961 | 10021 | 10021 | 80 | 10081 | 10141 8 | 7 6 | 10201 | ה דוסקסד | 10261 8 | 032 | 0321 | 0381 | | 2 . | • | 10441 | 10501 | TOTOL | TOCOL | 19501 | 10621 | 10621 | 10681 c | œ - | 10/41 0 | 7 7 | TOROT |
|---|----------|------------------------------|--------|----------------------|----------|--------|--------|--|---------------------------------------|--------------------------|--------|--------------------|-----------------------------|-------|--------------------|----------|----------------------|--------|----------|--------|---------------|---------|-------|----------------|---------------|---------|----------|----------|-------|------------------|---------|--------------|---------------|--------------|-------|
| QD | Qy | qq | Qy | qa | Qy | qq | Ωŷ | qa | Οy | qa | Οŷ | q | oy g | G (| g g | | y d | ò | 7 A | 1 8 | Š É | an o | δ | QQ · | Š Š | 2 6 | Š 7 | ar · | ΟŊ | q | ΩŊ | a a | ý f | 3 6 | δλ |
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| 8700 | 0 0 | 9/8 | æ | 882 | 000 | 888 | 894 | 94 | 2 | 0006 | 906 | 906 | 912 | 912(| 918 | 918 | 924 | 924 | 930(| 930(| 936 | 9360 | 942 | 9420 | 948 | 948 | 954 | 954 | 9600 | 96 | 9660 | 9660 | 9720 | 972 | |
| cactgg | 5 | ggrir ggttt | Ŧ | attt | 1 | JULI I | 10000 | | | 11111 11111 tqcqcq | ggcca | | tggga | - 5 | ggtcc | tggtcc | caggc | cagge | ctaagg | taagg | taactc | aactc | ctgac | tctgac | acaaa | acaaa | ttaat | tttaat | aaat | aaata | atcga | tatcga | ttact | ttaci | 44444 |
| 1 | א נ נ | Ligia ttqtac | 11133 | | 1 | 2 - 2 | | geete geete | + 55 | agg | , t, | — o | | aatgo | gat | gat | tttccttcaactccatcagg | tccat | tag | tag | ctg | ctg | aagat | taagat | itttgcaac | ttgca | ;; | tattt | agtg | agtga | tto | _ ;; | getta | 3ct | |
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| 111111 | 4 4 | actgad actgad | 99 | 3 = 1 | Č | acatt | aataa | 49699 agtgg | 7 | 11111 tcago | tttt | liliiii ttttagt | tgato | tgato | agcactgtgcctggtcca | gtcca | gcagctgt | | tttta | tttta | taget | taget | attt | | ttttgcat | tgcat | ۔ بند | ٽ ــ | tgtta | ijiii tgtta | agtgg | ttagtgg | atttcataaaagt | aaaag | |
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| | , , | <u>a</u> – a | Ö | , — B | , + | Coctqt | Lagge | | , פ | 11111 agtga | pagtt | JIIII | actec | actec | tgaago | gaage | cagaaat | | 8 = | | 200 | - 10 | ~~ | ~ | tttt | tttt | - 10 | tatgtgaa | ıaa | aaatat | taagt | | taatgtgat | taatg | |
| 1 | n r | gagcctgca gagcctgca | - 1 | tttagat | - 5 | 2 - 2 | , 50 | _ 5 _ 5 | , ‡ | ttcaagt | cacco | | rttc | ttte | ggegte | - g | gaattcac | a | ttcaaagt | بد٠ | acca | acca | tggt | ttggtcaa | gcttat | - rd | taaa | ctaaat | tttg | 111111 ttttga | | gaaag | ttgaa | ag | |
| | U T | Caatga caatga | Ď, | 4949 4141 agag | | | ctccat | ctccat | CCCAGO | CCagg | ccacca | ccaccac | ggctgg | gctg | ttacag | - g | ttta | ttttag | cťttat | ctttat | tctaac | tctaac | aaa | tgaaat | agtg | gtg | ttgt | tttgtc | ttga | gttgat | taat | ataato | tttatt | ttat | |
| 8641 | 202 | 8701 | 8761 | 8761 | 7 | 821 | - | 881 | 941 | 94 | 9001 | 9001 | 9061 | 9061 | 9121 | 9121 | 9181 | 9181 | 9241 | 9241 | 9301 | 9301 | 9361 | 9361 | 9421 | 9421 | 9481 | 9481 | 9541 | 9541 | 9601 | 9601 | 9661 | 9661 | |
| S | l è | 3 8 | ò | . a | è | 연 | 0 | . q | ò | : Q | δÿ | qq | οy | QQ | οy | Op | ογ | Ор | Οy | qq | δy | qa | δý | QQ | δý | QQ | δý | qq | δλ | QQ | ٥y | QQ | οy | QQ | |

| Db | 9721 | | 9780 |
|--------|-------|--|-------|
| Qy | 9781 | ttgataatctatatttatattgtctgatttttaaactgttttctatggtaatctttaa | 9840 |
| qa | 9781 | | 9840 |
| Oy | 84 | tegtatteetgettteeggaataggtaacagtgagcatgatgaaagtgacaageteact | 06 |
| qq | 9841 | cgtattcctgctttccggaataggtaacagtgagcatgatgaaaagtgacaagctcac' | 0066 |
| yo d | 9901 | tttacacactcgggcagttgccctattatcaggcagccgttcctgggggctgccagctgc | 0966 |
| 3 8 | 2 4 | C C | |
| d d | 9961 | egocotgoctttccatctccttccttgctgtcttctgcggctccttctgagggctgt | v 0 |
| Οy | 10021 | teactggattagectataaegectttecectettetaattaattgetgeteteaggt | 10080 |
| qa | 10021 | | 10080 |
| δλ | 10081 | aggttttggaaagcaataaagctgagctaggtcaagttccaggagtctcttggcatgagg | 10140 |
| qq | 10081 | ggttttggaaagcaataaagctgagctaggtcaagttccaggagtctcttggcatgag | 10140 |
| Qy | 10141 | acctgaaaaactcatctgttggaagacctcggctttgggcagctggtgcactgttggggc | 10200 |
| QQ | 10141 | cctgaaaaaactcatctgttggaagacctcggctttggggcagctggtgcactgttggggg | 10200 |
| Qy | 10201 | gttattggctgcgttctggctctcatcagtcttccagatactctgcattcctcagagagg | 10260 |
| qa | 10201 | ttattggctgcgttctggctctcatcagtcttccagatactctgcattcctcagagag | 10260 |
| QY | 026 | aacatatctccatgggttgagttcagctcccagggagatgggttccctgccttaagtcg | 032 |
| đ | 10261 | acatatctccatgggttgagttcagctcccagggagatgggtttccctgccttaagtc | 10320 |
| Qy | 10321 | gcaagtaccttttttttttttttgagacagagtctcgtctgtcaccaggctggagt | 10380 |
| qq | 10321 | caagtacctttttttttttttgagacagagtctcgctctgtcaccaggctggag | 10380 |
| Qy | 038 | | 044 |
| qq | 10381 | cagiggigcicatitggcicacigcaaccicigccicccagggicaagcagiicicci | 10440 |
| . Ογ | 10441 | cctcagcctcccgagtagctgggactacaggagcgcaccaccatgcccagctaattttg | 10500 |
| q | 10441 | ctcagcctcccgagtagctgggactacaggagcgcaccaccatgcccagctaatttt | 10500 |
| Qy | 10501 | attttttagtagagacggggtttcaccatgttggccaggatggtctggatctctt | 10560 |
| qq | 10501 | tttttttagtagagacggggtttcaccatgttggccaggatggtctggatctttg | 10560 |
| Qy | 10561 | tectgatecgectgecttggceteceaaagtgetgggattacaggegtgagecateat | 10620 |
| đ | 10561 | cctgatccgccttgccttcggcctcccaaagtgctgggattacagggggtgagccatca | 10620 |
| Qγ | 10621 | cagcetttatgtttetttgtttgttttgttttetgagatggagtccegetet | 10680 |
| qq | 10621 | ocagocittatgittittittittittittittittigagatggagtotogototgiti ocagocittatgittotttgittigittitgittittotgagatggagtotogototgiti | 10680 |
| Qy | 10681 | gctggagtgcagtgcatctcgacttactgcaacctctgccttcca | 10740 |
| qq | 10681 | caggctggagtgcagtgttgccatctcgacttactgcaacctctgccttccaggttca | 10740 |
| δδ | 10741 | gtgattccttgcctcagcctcccgtgtagctgggatcacaggtgcctgcc | 10800 |
| qa | 10741 | tgattccttgcctcagcctcccgtgtagctgggatcacaggtgcctgcc | 10800 |
| Qy | 10801 | gctaatttttgtattgttagtagacacagggtttcgccatgttggccaggctagtccga | 10860 |
| | | | |

| 86 | gt 10920 gt 10920 | tg 10980 tg 10980 | gc 11040 gc 11040 | ct 11100 ct 11100 | ic 11160 | c 11220 | it 11280 | 9 11340 - 9 11340 | ic 11400 | cc 11460 | t 11520 | aa 11580 aa 11580 | at 11640 | ta 11700 ta 11700 | ca 11760 | tc 11820 | cg 11880 | tg 11940 |
|--------------------------------------|--|--|---|--|--|--|--|---|--|--|--|--|--|--|---|--|---|---|
| gctaatttttgtattgttagtagacacagggtttcg | actcctgacctcaagtgatctgccttcctcagcctcctaaagtgctggggttacagga | gaaccaccatgcccagcettcaattaccttttatttatttatttatttatttattt | agacggagtctttctgtgttgcccaggctggagtgcggtgggcgcaatcttagctcactiiiiiiiiii | aacctcctccccaggctcaagtgattctcatgcatcagcttcccgagtagctggga | tcaggtgcccgccaccacttggctaattttgtgtttttagtagagacgggtttcac | catgitiggccaggctggtcttgaattictgacctcaaatgatcctcctgcttcagcctcctctcfctlagccaftll | caaagtgctgggattacaggcgtgagccactgccccaacagcaagtaccttttaaaca | tagagacatttagttgccatcctcaaacccgtttgggtgtgtgggagaatgttgggtcc | tgacatggttgttagttatctaaagatgtcagccatcaatca | actgaagctgtaatccttcatctaggatgatattttttaagatggaaaattctacaac | tgagaataaggatttcagatccaaatttgagactcagccctacgagtaactctttaact: | cagagagttaaaagaagatgcacagttgatgaagatttaaaggagaaaatggaaatca | tgtcatttagcactcaaagcctacatgtcatttctgacattttctgtttgtgtgaa | ttttttttcctataaaatgattgtgaagtttctggtagaattattgtttgcctttc | atgtaatagcatattagggtttttttttttttttttttt | <pre>ctctgtcgcccaggctggagtgcagtggcacgatctcgggtcactgcaatcttccgcc </pre> | ctgggttcctgcctcagcctccgagtagctgggactacaggcgcacgtcaccacacc | gctaatttttggtattttagtagtgacagggattcaccgtcttagccagggtggtct |
| 90 | 10861 | 10921 | 10981 | 11041 | 11101 | 11161 | 11221 | 11281 | 11341 | 11401 | 11461 | 11521 | 11581 | 11641 | 11701 | 11761 | 11821 | 11881 |
| qq | දු පු | Qy Db | Qy | Qy Dp | Qy Db | Qy | Qy Dp | Oy Dp | Oy Qa | Qy Dp | Qy Dp | Qy | Qy | Qy Db | Qy Dp | Oy Dp | Oy Op | ço qa |

| Qy | 11941 | tctcctgacctcatgatctacccgcctcggcttcccaaagtgctgggattacaggcat | |
|-----|-------|---|--|
| qq | 11941 | | |
| Qy | | 206 | |
| QQ | 12001 | googotgigoctggotattagagattttttattataatttatotocaagataaaagoag 120 | |
| δ | 1206 | agaaataaaaatcatccatgcttt 12 | |
| අ | 12061 | gacattatattgccacataattgaaaaatacaagagaaataaaaatcatccatgctttt 121 | |
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| q | 12241 | | |
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| ΩQ | | ttiattaaatttataatgagttaatgctgggaaataaaacactgatttaagtcattttg 1236 | |
| Οŷ | 12361 | cttttagtactaaagcatttgacaataaatgacttcttcagaatatggtataccttctg 1242 | |
| q | 123 | ttagtactaaagcatttgacaataaatgacttcttcagaatatggtataccttctg 124 | |
| Qγ | 12421 | caataaacgcattttaatgaattgtaaggaaacaacatcattttatttttatttt 1248 | |
| Q | 12421 | aagcaataaacgcattttaatgaattgtaaggaaacaaccatttttttt | |
| Qy | 12481 | gactttcgcttttgttgcctaggctggagtgcaatggcgcgatctcg 1254 | |
| qq | 4 | tttttgagacagactttcgcttttgttgcctaggctggagtgcaatggcggatctcg 1254 | |
| QY | 12541 | tectgagttg 126 | |
| QQ | 12541 | ctcactgcaacatccgcctctgggttcaagcgattctcctgcctcagcttcctgagttg 1 | |
| Qy | 12601 | ggattacaggcacgtgccaccacgcctggccaattttgtatttagtagagacgg | |
| QQ | 12601 | gggattacaggcacgtgccaccacgcctggccaattttgtatttttagtagagacg | |
| QY | 12661 | gtttctccacgttggtcaggctggtctcaaactcctgacctcaggtgatctgccgcctc 12720 | |
| qq | 12661 | ttictccacgitiggicaggetggitcicaaactectgaeeteaggigaicigeeegeete 1272 | |
| Qy | 12721 | cctccgaaagtactggaattacaggcgtgagccaccgtgcctggccaacattattatt 12 | |
| ф | 12 | goctocgaaagtactggaattacaggcgtgagccaccgtgcctggccaacattattit 1278 | |
| Οy | | ttttttaatctagaaaatacacttctaagaaaattgattaaaaccaacc | |
| qa | 12781 | titttaatetagaaaaataeaettetaagaaaattgattaaaaeeaaee | |
| Qy | 12841 | cccctaagatcacatctatgttctctttgttgcagcttcacttaaagaga | |
| qa | 12841 | gccctaagatcacatctatgttcttttgttgcagcttcacttaaagagagaaactt 1290 | |
| QY | 6 | tgetcaaagcaaaggagatgggeetcecagtgtgagtgtggggggtaaggettet 12 | |
| qa | 12901 | ttggtgctcaaagcaaaggagatgggcctcccagtgtgagtgtggggggtaaggcttct 1296 | |
| δŏ | 96 | tacacctgtccacttaaggaaatcacatttcacagaggccttgcct 130 | |
| qq | 12961 | gggactcactgggtacacctgtccacttaaggaaatcacatttcacagaggccttgcc | |

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cancer predisposing gene HPC2, which is found on chromosome 17p. Some alleles of this gene cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of cancer drugs. This sequence was isolated by cloning and sequencing the region of the genome which appeared to cause a predisposition to prostate cancer.
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                                                                           present sequence is the coding sequence of the human prostate
  cancer
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                                                                                                                                                                                                                                                                                                                                  Length 2958;
  prostate
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of
                                                                                                                                                                                                                                                                                                                                Score 657; DB 21;
Pred. No. 1e-204;
); Mismatches 0;
diagnosis
antibodies, useful for treatment and
                                  Claim 3; Page 98-100; 157pp; English
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Conservative 0;
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which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activitiess such as: cytostatic; hepatotropic; vulnerary;
sequences have activities such as: cytostatic; hepatotropic; vulnerary;
correspathic; antiparkinsonian; nootropic; neuroprotective;
costeopathic; anticonvulsant; antiarthritic; immunosuppressant;
finannostimulant; cardiant; thrombolytic; coaqulant; vasotropic;
controllabetic; hypotensive; dermatological; immunosuppressive;
antidiabetic; hypotensive; dermatological; in the presence of or predisposition to, or preventing or treating
the presence of or predisposition to, or preventing or treating
the presence of or predisposition to, or preventing or treating
the proteins and nucleic acids may be used to treat cancers,
proliferative disorders, neurodegenerative disorders, osteoarthritis,
cofraft vs host disease, cardiovascular disease, diabetes mellitus,
cofraft vs host disease, cardiovascular disease, diabetes mellitus,
cofraft vs host disease, candbined immunodeficiency (SCID), AIDS, viral,
bacterial or fungal infection, malaria, auticimmune disorders, asthma,
allergies, aplastic aneemia, burns, wounds, bone and cartilage damage,
nocturnal haemoglobinuria, antilifiammatory disease; to enhance
coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                  Authoraty; antipolatic; antiarthitic; immunosuppressant; cardiant; immunostimulant; osteopathic; antiarthitic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; encordences of antidiaped; antipolatic; part vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; asever condined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage antilnflammatory disease; coagulation;
                                                                                               cytostatic; hepatotropic; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               frame X,
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                              Human ORFX ORF2000 polynucleotide sequence SEQ ID NO:3999.
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                                                                                                  frame; ORFX; detection;
                                                                                                                              vulnerary; antipsoriatic; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 3179-3180; 5507pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombosis; contraceptive; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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Best Local Similarity 99.7
Matches 614; Conservative
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                                                                                                  open reading
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Gaps

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Indels

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2252 atagatgcctcttaggactggtgcctggcacagccgcgggccaggaggctgccacacgga 2311
                                                                                                                                                                                                                                                                                                                                                                              cgcacccgtatctgccctccttgctggtagaagctgaagagcacggtcccccaggaggca
                                                                                                                                                                             cgcacccgtatctgccctccttgctggtagaagctgaagagcacggtcccccaggaggca
                                                                                                                                                                                                                                          atagatgcctcttaggactggtgcctggcacagccgcgggccagaggctgccacacgga
                                                                                                                                                                                                                                                                                    agcaagcagatgaactaatttcatttcaaggcagtttttaaagaagtcttggaaacagac
                              cgggagctgcggcaggtgcgggcgcctcctgtccagggagctggcaggcggcctggag
                                                                                          SS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA52810 standard; cDNA; 2478 BP.
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human sulphatase G cDNA.
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30-JUN-2000; 2000WO-US18374
                      02-JUL-1999;
02-JUL-1999;
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                                                                    HXSE-)
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AAC27273
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                                                                                                                                                                                       contains 23 exons and is located at chromosome 17p11.2. The present sequence is clone lambda29.1 from a human testes CDNA library. It was isolated using human EST sequences with sequence similarity to the non-CTPSR family as a probe to screen the library. The cDNA insert was subcloned and the DNA sequence of both strands was determined. The sequence may be used to treat a patient suffering from hSG deficiency by replacing, repairing, or compensating for a DNA sequence within that
                                                                                                                                                                                                                                                                                                                                                                                                                970 accatatcgcaggcacccgcccgccgcggagcggccgcgcaaggacccgctgcggcacctg 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1030 cgcacgcgagagaagcgcggaccgtcggggtgctccgggcggcccaaacccgtgtacctg 1089
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                                                                          Novel isolated DNA sequence which encodes human sulfatase G or its fragment useful in gene therapy for treating patients suffering from
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                            1 atgtgggcgctttgctcgctgctgcggtccgcgggccggacgcatgtcgcagggacgc 60
                                                                                                                                           The present sequence encodes human sulphatase G (hSG). hSG is not a member of the well-characterised CTPSR sulphatase family. It belongs to a family showing sequence similarity to a sulphatase from the marine bacterium Alteromonas carrageenovora. The hSG gene
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                                                                                                                                                                                                                                                                                                                          Length 2478;
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100.0%; Pred. No. 2e-71;
ive 0; Mismatches 0;
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(WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
                                                                                                                      Claim 2; Page 29-30; 33pp; English.
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                      Hopwood JJ, Litjens T,
                                                                                                 sulfatase deficiency
                                         WPI; 2000-431273/37
                                                                                                                                                                                                                                                                                                                                     Local Similarity
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241 aaccggt 247
                                                      P-PSDB; AAY99850
                                                                                                                                                                                                                                                                    patient's genome
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Lamson G, Drmanac R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                            Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                 Innis MA, Garcia PD, Klinger J, Ki
Kennedy GC, Pot D. Lamson G, Drman
Dickson M, Labat I, Leshkowitiz D;
LW, Strache-Crain B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 386 BP; 82 A; 90 C; 111 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26627 ctcagagagccacccttattcgccaagtcttttgaca 26664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 158; DB 22;
Pred. No. 2.5e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein 5' EST, SEQ ID NO: 31348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page 550-551; 1046pp; English.
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99US-0142310.
99US-0142311.
                                                                                                                                          Williams LT, Esconeuc Reinhard C, Randazzo F, 'Ronnanac S, 'L' Press
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                                                                                                                                                                                                                                                       Jones
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                                                                                                                                                                                                                                                                                                        WPI; 2001-091805/10.
                                                                                      CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                    García V,
                                                                                                                HYSEQ INC.
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Key
                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTRN of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 183 BP; 36 A; 63 C; 38 G; 46 T; 0 other;
                                                                                                                                                                                             Giordano J;
                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 31348; 71pp + CD-ROM; English.
                                                                                                                                                                                                Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression and secretion vectors.
                                                             21-FEB-2000; 2000EP-0200610,
                                                                                                      99US-0122487
                                                                                                                                                                                                Dumas Milne Edwards J,
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Query Match 0.5%; Score 143; DB 21; Length 183; Best Local Similarity 100.0%; Pred. No. 2.2e-37; Matches 143; Conservative 0; Mismatches 0; Indels (
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Polymorphic repeat microsatellite sequences present in the CTLA4 locus
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                                                                                                                                                                                    Autoimmune disease; polymorphic microsatellite repeat; PMR; CD28 gene;
                 AAA96365 standard; DNA; 50000 BP
                                                                                                  08-FEB-2001 (first entry)
                                                         AAA96365;
AAA96365/c
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Homo sapiens.

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Two human bacterial artificial chromosome (BAC) clones that included and flanked the human CTLA-4 locus were cloned and sequenced. The sequence data was assembled into a contiguous sequence that is presented in AAA96363-68. AAA96363-64. Comprise BAC clone 22700, and AAA96365-68 comprise BAC clone 22700, and AAA96365-68 microsatellite repeat (PMR) sequences contain polymorphic microsatellite repeat (PMR) sequences. The specification describes a method for determining the predisposition of a human subject to develop autoimmune disease. The method comprises detecting a PMR sequence in the CD28, ICOS gene or CTLA4 gene of the human costimulatory receptor gene locus (HCGRL). PMR sequences vary in length among individuals and can be amplified to generate products that differ in size. These products can then be detected by rapid and convenient high resolution processes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining predisposition of humans to develop autoimmune disease involves detecting polymorphic microsatellite repeat sequence within human costimulatory receptor gene locus
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/note= "sarall/12 microsatellite repeat"
26009..26056
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15527..15567
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/note= "sara15/16 microsatellite repeat"
30069..30101
                                       "sara39/40 microsatellite repeat"
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24050..24075
                                                                                                                                                                                                                                                         sara13/14 microsatellite repeat"
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                                                                                  "sara33/34 microsatellite repeat"
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46547..46572
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43819..43925
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/note= "sara7/8 microsatellite repeat"
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Location/Qualifiers
                                         /note= "sara
11459..11520
                                                                                              12329..12419
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30535..30574
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33714..33758
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27317..27
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99WO-IB01353.

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(GEST ) GENSET
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 23-JUL-1999;
                                      23-JUL-1998;
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method is useful for determining the predisposition of insulin-dependent
           diabetes mellitus (IDDM), Addison's disease, Graves disease, autolmmune hypothyroidism, myasthenia gravis, thymoma, lupus, thyroiditis, postpartum thyroiditis, rheumatoid arthritis, Hashimoto's disease, coeliac disease and leprosy. PMR sequences within hCRGL are useful as markers in a variety of assays and in the field of forensic medicine, disease diagnosis and human genome mapping.
                                                                                                                                                                                                                                                                                                    Db 48846 TGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGATAGTCTCGATCTTTAGT 48787
                                                                                                                                                                                                                                                                                4719 tgtatttttagtagagaggggtttcaccatgttggccaggatagtctcgatctttgac 4778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding a human geranylgeranyl pyrophosphate synthetase (hGGPPS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; geranylgeranyl pyrophosphate synthetase; hGGPPS; chromosome 1; 1q42-1q43 locus; prostate cancer; hGGPPS; biallelic marker; mevalonic biosynthetic pathway; ss.
                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                  Sequence 50000 BP; 14509 A; 9641 C; 10130 G; 15720 T; 0 other;
                                                                                                                                                                                                          Score 84; DB 21; Length 50000;
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                            1.1e-18;
                                                                                                                                                                                                      Query Match 0.3%; Score 84; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 84; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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827..7191
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7385..13759
/*tag= f
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13760..13830
/*tag= g
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/*tag= h
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14063..15251
/*tag= i
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7292..7384
/*tag= e
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/number= 1
633..826
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547..7291
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The present sequence represents a genomic sequence of human geranylgeranyl pyrophosphate synthetase (hGGPS). The sequence comprises the 5' regulatory region, the exons and introns, and comprises the 5' regulatory region. Two differently spliced mRNAs exist for this gene. The first spliced mRNA is derived from a cDNA (AAZ60888) which comprises lbis, 2, 3 and 4. The second mRNA is derived from a cDNA (AAZ60889) which comprises lbis, 2, 3, and 4. The hGGPPS gene is located on chromosome 1, at the 1442-1443 locus. This chromosome 1 locus has been shown to carry a predisposing gene for prostate cancer. The nucleic acids encoding hGGPPS can be used for screening for agents which modulate the expression of the hGGPPS gene. Such agents which modulate the expression of the hGGPPS gene. Such agents the hGGPPS gene can be used for the diagnosis of diseases related to an alteration in the regulatory or coding regions of hGGPPS, such as pathologies related to a defect in the mevalonic biosynthetic pathway.
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5.4e-16;
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98US-0093940.
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Best Local Similarity
Local 76; Conserva
                                                                                                                                                                                                       WPI; 2000-182704/16.
P-PSDB; AAY68909.
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ94762;
                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                     vectors.
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                                                                                                                                                                   AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from the human colorectal adenocarcinoma (colon cancer) cell line SW480. The cDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                    present in a human tumour, particularly in solid tumours, e.g. carchiomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia,
                                                                                                                                                                                                                                                                                                                                                  1085 acctgcaggtggtggcagcgggtagccgggactcgggcgccgcgctctacgtcttctccg 1144
                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                          Novel nucleic acids, used to develop products for the diagnosis and treatment of disorders involving unwanted cell proliferation, particularly cancers, especially colon cancer
                                                Bushnell SE;
4E, Monahan JE;
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                                                                                                                                                                                                                                                                                                           Length 238;
                                                                                                                                                                                                                                                                                                                              Indels
                                                KE, Astle JH, Burgess CC, Bus
Derti A, Ford DM, Lewis ME,
                                                                                                                                                                                                                                                                                                           DB 21; L
2.5e-14;
                                                                                                                                                                                                                                                                              Sequence 238 BP; 55 A; 57 C; 69 G; 57 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein 5' EST, SEQ ID NO: 2518.
                                                                                                                                                                                                                                                                                                          0.3%; Score 72; DB 100.0%; Pred. No. 2.5 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; chromosome mapping; ss
                                                                                                                                                Claim 15; Page 258; 469pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC02520 standard; cDNA; 215 BP
          98US-0088801
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                                                                                                                                                                                                                                                            dysplasia or hyperplasia.
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                                                Steinmann KE
Catino TJ,
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                                                                                                                                                                                                                                                                                                                                                                                         1145 agttcaaccggt 1156
                                                                                                                                                                                                                                                                                                                                                                                                           61 agttcaaccggt 72
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                                                                                       WPI; 2000-087220/07
                            (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 72; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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          10-JUN-1998;
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                                                                   Schlegel R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC02520;
                                                                                                                                                                                                                                                                                                            Query Match
                                                Endege W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human;
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8353 agaagagatagcagatcttcagaaaagctgatggaaggccgggtgcagtggctcacgcct 8412
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                                     obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABCG1; ABC8; ATP binding cassette; human; phagocyte; cholesterol; phospholipid; transporter; inflammation; atherosclerosis; lipid disorder; dyslipidemia; psoriasis; lupus erythematosus; diagnosis; gene therapy; chromosome 21q22.3; ss.
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                                                                                                                                                          Claim 1; SEQ ID 2518; 71pp + CD-ROM; English.
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Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adenosine triphosphate binding proteins useful for identifying agents for treating atherosclerosis and other inflammatory disorders ^{\rm -}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                     for diagnostic and therapeutic applications, and for biochemical or call-based assays to screen for pharmacologically active compounds useful for the treatment of lipid disorders, atherosclerosis or other inflammatory diseases such as psoriasis and lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABCG1; ABC8; ATP binding cassette; human; phagocyte; cholesterol;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phospholipid; transporter; inflammation; atherosclerosis;
lipid disorder; dyslipidemia; psoriasis; lupus erythematosus;
diagnosis; gene therapy; chromosome 21q22.3; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                    Sequence 2923 BP; 593 A; 873 C; 803 G; 641 T; 13 other;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 60; DB 21; I
Pred. No. 1.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                   erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                       Gaps
           ABCG1 is the human homologue of the Drosophila white gene.
Sequencing of the promoter revealed important transcription factor
binding sites relevant for phagocytic differentiation and lipid
sensitivity. ABCG1 was also identified as a cholesterol
transporter and modulator of choline-containing phospholipids
(phosphatidylcholine, sphingomyelin). The invention provides
cholesterol-sensitive ABC genes (see AAC94734-63) that can be used
for diagnostic and therapeutic applications, and for biochemical useful for the treatment of lipid disorders, atherosclerosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; interleukin 1; IL-1B; IL-1R; IL-1RN; diagnosis; detection; chronic obstructive airway disease; chronic bronchitis; emphysema; asthma; chronic bronchiolitis; proinflammatory haplotype; ss.
completely set back to differentiation dependent levels by HDL3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genotyping nucleic acid samples for interleukin-1 (IL-1) proinflammatory haplotype alleles, useful for predicting susceptibility to developing chronic obstructive airway disease
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                                                                                                                                                                                                                                                                                                 0.2%; Score 60; DB 21; Length 2923; 100.0%; Pred. No. 1.2e-10; Ative 0; Mismatches 0; Indels 0
                                                                                                                                                                                           other inflammatory diseases such as psoriasis and lupus
                                                                                                                                                                                                                                                Sequence 2923 BP; 593 A; 873 C; 803 G; 641 T; 13 other;
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ID AAX75924 standard; DNA; 9721
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97GB-0023553.
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                                                                                                                                                                                                                                                                                                                       Similarity
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07-NOV-1997;
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Best Local Simi
Matches 60;
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                disease or for predicting the rapidity or ultimate progression of chronic obstructive airway disease (COAD). COAD can be asthma, emphysema, chronic bronchitis or chronic bronchilits. The method provides for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Low adenosine antisense oligonucleotide; phosphorothicate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma: RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and

      QY
      11740 ttttttgagacagatctcactctgtcgcccaggctggagtgcagtggcacgatctcgg
      11799

      DD
      956 TTTTTTTGAGACAGAGTCTCACTCTGTCCCCCAGGCTGGAGTGCAGTGCCAGGCACGGCGG
      897

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the susceptibility of subjects to developing chronic obstructive airway
                                                                                 early identification of chronic obstructive airway disease (COAD), facilitating administration of appropriate treatment at the earliest stage, thereby increasing the probability of a positive outcome. The present sequence represents the human IL-1B gene.
                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                        DB 20; Length 9721;
                                                                                                                                                                                                    Sequence 9721 BP; 2662 A; 2328 C; 2121 G; 2608 T; 2 other;
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human interleukin-1 polynucleotide fragment #2512.
                                                                                                                                                                                                                                                                   0.2%; Score 60; DB 20; I
100.0%; Pred. No. 9.5e-11;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 230-232; 1592pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF20945 standard; DNA; 9721 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                      Query Match 0.2
Best Local Similarity 100.
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-679539/66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF20945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nyce JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, ONS and peripheral nervous and non-nervous system receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease condition selected from pulmonary vasoconstriction, inflammation, allergyies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic thinitis (AR), pulmonary condition emphysema, chronic obstructive pulmonary distress syndrome (Appertunction).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for predicting the risk of interstitial lung disease, comprising detecting an interleukin-1 receptor antagonist allele and tumor necrosis alpha allele or an allele in linkage disequilibrium with
                                                                                                                                                                                                                                                                                                                                                                                                            fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11740 tttttttgagacagagtctcactctgtcgcccaggctggagtgcagtggcacgatctcgg 11799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; IL-1B; interleukin-1B; cytostatic; antiinflammatory; immunosuppressive; dermatological; antimicrobial; antiarthritic; IL-1 receptor antagonist; tumour necrosis factor alpha antagonist interstitial lung disease; interstitial pneumonia; pulmonary fibrosis; rheumatoid arthritis; systemic lupus erythmatosis; Sjogren's syndrome; systemic sclerosis; dermatomyocitis; chromosome 2; ds.
                                                                                                                                                                                                                                                                                                                                                                   pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.2%; Score 60; DB 21; Length 9721;
100.0%; Pred. No. 9.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match V. **, - Fred. No. 9.5 Best Local Similarity 100.08; Pred. No. 9.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whyte M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INTE-) INTERLEUKIN GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC63768 standard; DNA; 9721 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Fig 2; 102pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    either of these alleles
                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-656234/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human IL-1B gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200060117-A2.
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       The present sequence is provided in a specification relating to a method for determining whether a subject has or is predisposed to develop an interstitial lung disease. The method involves detecting an interleukin-1 receptor antagonist (IL-IRN) (+2018) allele 2, a tumour necrosis alpha (TNF-A)(-308) allele 2, or an allele in linkage disequilibrium with either of these two alleles. The method may be used to determine whether a subject has or is predisposed to develop an interstitial pneumonia or a pulmonary fibrosis and other disorders such as rheumatoid arthritis, asystemic lupus exythmatosis, Sjogren's syndrome, systemic sclerosis, dermatomycoitis. The method is also used for identifying molecules which can be used as therapeutics for treating interstitial lung disease.
                                                                                                                                                                                                                                             Novel methods and nucleic acids for diagnosing and treating disorders associated with high levels of interleukin lbeta, especially
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-1 beta; IL-1B; human; polymorphism; inflammation; coronary artery disease; osteoporosis; nephropathy; alopecia areata; Graves disease; systemic lupus erythematosus; lichen sclerosis; ulcerative colitis; diabetic retinopathy; periodontal disease; juvenile chronic arthritis; psoriasis; insulin dependent diabetes; asthma; lung fibrosis; chronic inflammatory lurer disease; rheumatory corteoperesity chromic inflammatory lung disease; antiinflammatory; osteopathic; dermatological; immunosuppressive, antidiabetic; antithyroid; antiarthritis; antithemmatic; antiasthmatic; antipsoriatic; hepatotropic; antiulcer; diagnosis; therapy; ds.
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                                                                                                                                                                                               Length 9721;
                                                                                                                                                          Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;
                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                              0.2%; Score 60; DB 21; I Similarity 100.0%; Pred. No. 9.5e-11; 00; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "IL-1B allele 1 (+6912)"
                                                                                                                                                                                                                                                                                                                                                                                                            Human interleukin-1 beta allele 1 (+6912).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
replace(8904,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INTE-) INTERLEUKIN GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 74pp; English
                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                  AAA50174 standard; DNA; 9721
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                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-558192/51.
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                                                                                                                                                                                                                       90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variation
                                                                                                                                                                                                                                                                                                                                                            AAA50174;
                                                                                                                                                                                            Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                      AAA50174/c
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                                                                                                                                                                                                                       Matches
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The present sequence is that of human interleukin-1 beta (IL-1B)
allele 1 (+6912), which is a form of the IL-1B gene that contains
cytosine at position (96212). IL-1B allele 2 (+6912) has guanhe at
this position (see AAA50175). The invention is based on the
identification of this novel allele at marker +6912 of the IL-1B
gene. The C to G transition occurs within the 3' untranslated
cregion of the IL-1B gene and results in an increased level of IL-1B
protein. Individuals homozygous for the IL-1B allele 2 (+6912)
credion of the IL-1B gene and results in an increased level of IL-1B
protein. Individuals homozygous for the IL-1B allele 2 (+6912)
ccumulate approximately 4 times more immunoreactive IL-1B protein
than homozygotes for IL-1B allele 1 (+6912), or an allele in
than homozygotes for IL-1B allele 2 (+6912), or an allele in
provided for detecting IL-1B allele 2 (+6912), or an allele in
linkage disequilibrium with an IL-1B allele 2 (+6912), and
thereby determining a patient's susceptibility to developing
inflammatory disorders, especially coronary artery disease,
osteoporosis, nephropathy in diabetes mellitus, alopecia areata,
craves disease, systemic lupus erythematosus, libens acclaroals,
uvenile chronic arthritis, psoriasis, insulin dependent diabetes,
the protein of the IL-1B allele 2 (+6912) and its involvement in
IL-1B overproduction also eables screening assays for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IL-IB antagonists that can be used to treat conditions associated with IL-IB allele 2 (+6912). Transgenic animals are also claimed, and can be used to identify IL-IB agonists and antagonists, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              periodontal disease; juvenile chronic arthritis; psoriasis; insulin dependent diabetes; asthma; lung fibrosis; chronic inflammatory liver disease; rheumatord arthritis; chronic inflammatory lung disease; antiinflammatory; osteopathic; dermatological; immunosuppressive; antidiabetic; antithyrold; antiarthritic; antirheumatic; antiasthmatic; antipsoriatic; hepatotropic; antiuleur; diagnosis; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin-1 beta; IL-1B; human; polymorphism; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to confirm the safety and efficacy of candidate therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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9.5e-11;
hes 0;
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/note= "IL-1B allele 2 (+6912)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human interleukin-1 beta allele 2 (+6912).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 60;
Pred. No.
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replace(8904,C)
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Best Local Similarity 100.0%; Pr
Matches 60; Conservative 0;
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99WO-US17712. 98US-0095212.

03-AUG-1999; 03-AUG-1998;

24-FEB-2000

WO200009525-A2. Homo sapiens.

(UYEC-) UNIV EAST CAROLINA.

WPI; 2000-205971/18.

Nyce JW;

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The present sequence is that of human interleukin-1 beta (TL-1B) allele 2 (+6912), which is a form of the IL-1B gene that contains guanine at position (see AA5014). The allele 1 (+6912) has cytosine at this position (see AA5014). The invention is based on the identification of this novel allele at marker +6912 of the IL-1B gene. The C to G transition occurs within the 3' untranslated region of the IL-1B gene and results in an increased level of IL-1B protein. Individuals homozygous for the IL-1B allele 2 (+6912) accumulate approximately 4 times more immunoreactive IL-1B protein than homozygotes for IL-1B allele 1 (+6912), or an allele in provided for detecting IL-1B allele 2 (+6912), and thereby detecting IL-1B allele 2 (+6912), and linkage disequilibrium with an IL-1B allele 2 (+6912), and linkage disequilibrium with an IL-1B allele 2 (+6912), and inflammatory disorders, especially coronary artery disease, osteoporosis, nephropathy in diabetes mellitus, alopecia areata, of Gaves disease, systemic inpus erythematosus, lichen sclerosis, ulcerative colitis, diabetic retinopathy, periodontal disease, juvenile chronic inflammatory liver disease, colitis, diabetic retinopathy, periodontal disease, then disease, lung fibrosis, and rheumatoid arthritis (claimed): IL-1B netagonists that can be used to treat conditions associated with IL-1B allele 2 (+6912) and its involvement in IL-1B antagonists colaimed, with IL-1B allele 2 (+6912) and antagonists, or and can be used to identify IL-1B agonists, or
                                                                                                                                                                                                                                         Novel methods and nucleic acids for diagnosing and treating disorders associated with high levels of interleukin lbeta, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              confirm the safety and efficacy of candidate therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.2%; Score 60; DB 21; Length 9721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9721 BP; 2661 A; 2327 C; 2123 G; 2608 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 9.5e-11;
                                                                                            (INTE-) INTERLEUKIN GENETICS INC.
                                                                                                                                                                                                                                                                                                                                        Claim 34; Fig 2; 74pp; English
10-FEB-2000; 2000WO-US03443.
                                               99US-0247874.
                                                                                                                                           Di Giovine FS;
                                                                                                                                                                                                                                                                                           inflammatory diseases -
                                                                                                                                                                                          WPI; 2000-558192/51.
                                               10-FEB-1999;
                                                                                                                                           Duff GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Gaps ö 0; Indels 100.0%; Pred. ... Best Local Similarity 100. Matches 60; Conservative

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Qy 11740 tttttttgagacagagtctcactctgtcgcccaggctggagtgcagtggcacgatctcgg 11799

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Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstitction; inhibitor; antinflammatory; antiallergic, antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                              Human adenosine receptor related polynucleotide SEQ ID NO:2512.
                                                AAA34823 standard; DNA; 9721 BP.
                                                                                                                                             28-JUL-2000 (first entry)
18
                       AAA34823/
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IL-1; interleukin; inflammation; infection; ds.

(first entry)

02-APR-2001

IL-1B DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation. The ON can have antilinflammatory, antiallergic, antialergic, antialergic, antialergic, oytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasconstriction, allergies, asthma, impeded respiration, respiratory distances syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary diseases (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONS reduces down with the release of decyydenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA33312 represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID No:1 to 2815, and then the last 185 sequences are also called SEQ ID No:1 to 185, but the sequences differ from the previously named sequences. SEQ ID No:11 to 1680 (AAA33333 to AAA3992) are specifically claimed ONs from the present invention N. B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy 11740 tttttttgagaacagagtctcactctgtcgcccaggctggagtgcagtggcacgatctcgg 11799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                   New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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100.0%; Pred. No. 9.5e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 673-675; 1343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF27666 standard; DNA; 9721 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF27666;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a new method for determining whether a subject has or is predisposed to developing a disease or condition that is associated with an IL (interleukin)-1 inflammatory haplotype, comprises detecting at least one allele of the haplotype, where the presence of the allele indicates that the subject is predisposed to the development or has the disease or condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; IL-1A; interleukin-lalpha; IL-1B; interleukin-lbeta; IL-1RN; interleukin-1 receptor antagonist; vasotropic; antiinflammatory; hypotensive; anticoaqulant; antilipaemic; arterial restenosis; restenosis associated allele; RAA; occlusive cardiovascular disorder; restenosis detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                           Determining whether a subject has or is predisposed to disease associated with IL-1 polymorphism involves determining presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2607 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.2%; Score 60; DB 22; Length 97;
100.0%; Pred. No. 9.5e-11;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           marker or allele comprising it-1 inflammatory haplotype
                                                                                                                                                                                                                          Camp NJ, Di Giovine FS;
                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 4; 84pp; English.
                                                                                                                                                                                          (INTE-) INTERLEUKIN GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human IL-1B nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC91434 standard; DNA; 9721
                                                                                                                    30-JUN-2000; 2000WO-US18318
                                                                                                                                                        99US-0345217
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Best Local Similarity 100.4
Matches 60, Conservative
                                                                                                                                                                                                                                                         WPI; 2001-102903/11.
                                                                                                                                                                                                                        Duff GW, Cox A,
                                                 WO200100880-A2
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                 Unidentified
                                                                                                                                                    30-JUN-1999;
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                                                                                     04-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; II-1 receptor complex; BAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oy 11740 ttttttttgagacagagtctcactctgtcgcccaggctggagtgcagtggcacgatctcgg 11799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                956 ITITITITIGAGACAGAGTCTCACTCTGTCGCCCAGGCTGGACTGCAGGCACGATCTCGG 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                 Diagnosing or determining susceptibility to developing restenosis involves detecting restenosis associated allele in a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                  Stephenson K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;
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                                                                                  Francis SE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Prec. ....
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                                                                                  Crossman DC,
                                                                                                                                                                                                                      Disclosure; Fig 2; 129pp; English.
                                                 (INTE-) INTERLEUKIN GENETICS INC
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              99US-0431352.
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99US-0317674
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                                                                                  Duff GW,
                                                                                                                WPI; 2001-025173/03
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Best Local Similarity
Matches 60; Conserv
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24-MAY-1999;
               01-NOV-1999;
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                                                                                  Kornman KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX02996;
                                                                                                                                                                                        sample
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WO200062736-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF20950;
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                                                                                    AAX02956-X03048 and AAX22301-X22304 are overlapping BAC genomic sequences containing alternatively spliced forms of human IL-Ira. Such fragments are used in the method of the invention which describes the isolation of a novel human TAMO-77 encoding nucleic acid and protein. Tango-77 is a member of the cytokine superfamily that is expected to Inhibit inflammation by binding to the interleukin-1 receptor (IL-IR). It may also bind to a new receptor so could regulate other cellular processes associated with acute or chronic inflammation, e.g. asthmatchnic myelogenous leukaemia, rheumatoid arthritis, psoriasis and chronic myelogenous leukaemia, rheumatoid arthritis, psoriasis and cytokines and growth factors. Modulators of this protein are used to treat or prevent conditions associated with abnormal levels of inflammation, or activity of IL-1 or its receptor complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX02956-X03048 and AAX22301-X22304 are overlapping BAC genomic sequences containing alternatively spliced forms of human IL-Ira. Such fragments are used in the method of the invention which describes the isolation of a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a member of the cytokine superfamily that is expected to
solated nucleic acid encoding the new human cytokine Tango-77 to inhibit inflammation and to screen for specific modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding the new human cytokine Tango-77 used to inhibit inflammation and to screen for specific modulators
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                                                                                                                                                                                                                                                                                                                                                                                                        0.2%; Score 60; DB
100.0%; Pred. No. 9.4
:ive 0; Mismatches
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                                                      Example 5; Figure 3; 226pp; English.
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97US-0054646.
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nes 60; Conserv
   isolated
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04-AUG-1997;
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Matches
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inhibit inflammation by binding to the interleukin-1 receptor (IL-IR). It may also bind to a new receptor so could regulate other cellular processes associated with acute or chronic inflammation, e.g. asthma, chronic myelogenous leukaemia, rheumatoid arthritis, psoriasis and inflammatory bowel disease. It may also induce or suppress interleukins, eytokines and growth factors. Modulators of this protein are used to treat or prevent conditions associated with abnormal levels of inflammation, or activity of IL-1 or its receptor complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pain; cystic fibrosis; allergic rhinitis; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Low adenosine (A) content antisense oligonucleotides which do not triqqer adenosine receptors during metabolism, useful e.g. for tre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 14690;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14690 BP; 3810 A; 3245 C; 3299 G; 4327 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trigger adenosine receptors during metabolism, useful e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human interleukin-1 polynucleotide fragment #2517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.2%; Score 60; DB 20; L
100.0%; Pred. No. 8.8e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 221-227; 1592pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancers and respiratory obstructions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF20950 standard; DNA; 29433 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAR-2000; 2000WO-US08020.
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J W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.2
Best Local Similarity 100.
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-679539/66.
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transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonuclectides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors. CNS and peripheral nervous and non-nervous system peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention.
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Sequence 29433 BP; 8714 A; 6519 C; 5920 G; 8278 T; 2 other;

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                                                                                                                           Qy 11740 tttttttgagacagagtctcactctgtcgcccaggctggagtgcagtggcacgatctcgg 11799
                                                                                                                                                                Db 14423 TTTTTTGAGACAGAGTCTCACTGTGCCCCAGGCTGGAGTGCCAGTGGCACGAGTCGC 14364
                                                                      Gaps
                                                                  ;
Query Match 0.2%; Score 60; DB 21; Length 29433; Best Local Similarity 100.0%; Pred. No. 7.6e-11; Matches 60; Conservative 0; Mismatches 0; Indels 0
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Human adenosine receptor related polynucleotide SEQ ID NO:2517. AAA34828 standard; DNA; 29433 BP 28-JUL-2000 (first entry) AAA34828; AAA34828/ TO DE STATE OF STATE

antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss. Human; adenosine receptor; low adenosine antisense oligonuclectide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

Homo sapiens.

WO200009525-A2.

24-FEB-2000

98US-0095212. 99WO-US17712. 03-AUG-1999; 03-AUG-1998;

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

WPI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers

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The present invention describes a new composition comprising an antisense oligonuclectide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergites, and/or inflammation. The ON can have antiinflammatory, antiallergites, and/or confidence acids involved in bronchoconstriction, allergites, and/or antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation.

Consequence afflict the lungs of a subject. They can be used for treating e.g. ischemic conditions, pulmonary vasconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive carbinary disease (CODP), and cancers such as leukammias, impediance ancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONS break down with the crease of deoxyadenosine which activates adenosine receptors causing conclude sequences given in the sequence listing from the present to invention, which correspond to SEQ ID NO:1 to 2815, but the sequences of differ from the previously named sequences. SEQ ID NO:1 to 1885, but the present content of invention AAA3333 to AAAA3333 to AAA3333 to AAA3333 to AAA3333 to AAA3333 to AAA3333 to A
                               Disclosure; Page 677-684; 1343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        given in the sequence listing.
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Gaps ; 0 Length 29433; Indels DB 21; L 7.6e-11; ö ilarity 100.0%; Pred. No. 7.6 Conservative 0; Mismatches 0.2%; Score 60; 00.0%; Pred. No. Query Match Best Local Similarity Watches 60; Conserv

Sequence 29433 BP; 8714 A; 6519 C; 5920 G; 8278 T; 2 other;

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RESULT 25

AAF21437/c ID AAF21437 standard; DNA; 209273 BP

AAF21437;

(first entry) 14-MAR-2001 Human factor-related antisense polynucleotide #3004.

human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; pulmonary dispiratory distress syndrome; pain; cystic fibrosis; allergic rhintis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; Low adenosine antisense oligonucleotide; phosphorothioate; allergy; cancer; ss.

Homo sapiens.

WO200062736-A2.

26-OCT-2000.

24-MAR-2000; 2000WO-US08020.

99US-0127958. 06-APR-1999;

(UYEC-) UNIV EAST CAROLINA

Giordano J;

Nyce JW;

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs 5' ESTs are also used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leucocyte specific transcript; LST-1; cytokine; immunoregulator; lymphoma; U-937; antitumour; tumour; gene therapy; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 310 BP; 69 A; 74 C; 87 G; 76 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human leucocyte specific transcript LST-1 gene.
                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID 25339; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 59; DB 2
; Pred. No. 4e-1
0; Mismatches
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                                                                                                                                                    Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/note= "exon 1A"
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/note= "exon lB"
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21-FEB-2000; 2000EP-0200610.
                                                 99US-0122487
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1044..1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.2%
Best Local Similarity 100.0
Matches 59; Conservative
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544..652
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                                                                                                                                                    Dumas Milne Edwards J,
                                                                                                                                                                                                   WPI; 2000-500381/45.
                                                                                                  (GEST ) GENSET
                                                 26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes low adenosine (A) content antisense oligonuclectides and compositions (I) comprising them. In the antisense oligonuclectides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodiator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonuclectides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and malignancies, such as stimulating and crivating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adenosine receptors, bradykinin receptors, central chemokine receptors, adenosine receptors, bradykinin receptors, central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptors, CNS and peripheral nervous and non-nervous system peptides transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or lung inflammation, alleray(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiratory distress syndrome (C RDS), pain, cystic fibrosis (CT), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAR18434 to AAR21843 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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gene therapy; chromosome mapping; ss.
                                                                                                                                            Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy 11740 tttttttgagaacagagtctcactctgtcgcccaggctggagtgcagtggcacgatctcgg 11799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 209273 BP; 59273 A; 45843 C; 42459 G; 61176 T; 522 other;
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                                                                                                                                                                                                                                               Disclosure; Page 55-100; 1592pp; English.
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Best Local Similarity 100.0
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention
                                                                                                WPI; 2000-679539/66.
(NYCE/) NYCE J W.
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AAC21264;

RESULT 26 AAC21264

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DB 21; Length 310; 4e-10; 0; Indels

intron

exon

intron

exon

intron

exon

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"in exon 5, after position 2345, there is an internal 5' donor splice site; alternative splicing yields a 97-aa LST-1 isoform"
                                                                                                                      interferon-gamma; immunoregulatory protein; tumour; cancer; metastasis; cell proliferation; marker; leukaemia; diagnosis;
                                                                                                          LST-1; leukocyte specific transcript-1; cytokine; U937 cell;
                                                                                   Human LST-1 (leukocyte specific transcript-1) gene.
                                                                                                                                                                                                location/Qualifiers
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                                                                                                                                                                                                                                                                             /*tag= c
/~t+e= "exon 1B"
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"exon 4"
                                                                                                                                                                                                                        '*tag= a
'note= "exon 1A"
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exon 3"
AAT45451/c
ID AAT45451 standard; DNA; 5581 BP.
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'note= "exon 2"
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2345
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/*tag= ''
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/*tag=
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1044..1162
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/*tag= f
1475..1567
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544..652
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P-PSDB; AAW07680.
                                                                                                                                                gene therapy; ds.
                                                                                                                                                                        Homo sapiens
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                                                           06-APR-1997
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                                    AAT45451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A genomic DNA sequence (AAT48737) codes for a novel cytokine-like protein, leucocyte specific transcript LST-1 (AAW10880), whose prodn. C by human lymphoma U-937 (DSM ACC 5) cells is stimulated more than 100-fold by interferon-gamma and which binds to the surface of eucocytes. The gene was obtd. by screening cosmid library cah, c produced from human B cell line CAH genomic DNA, with a TNFA probe. Plasmid pLST-1 contg. the LST-1 gene has been deposited as DSM (10011. LST-1 genomic DNA or cDNA (see also AAT48738) can be used to produce recombinant LST-1 in prokaryotic or eukaryotic host cells. LST-1, opt. generated in vivo from DNA constructs, is useful as an immunoregulatory and antitumour agent, esp. as it modulates co-operation between T cells and macrophages. LST-1 DNA can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New immunoregulatory protein, LST-1, derived from human lymphoma cell line - binds to the surface of leucocytes, useful for treatment and diagnosis of tumours
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"IFN-stimulated gene factor-2 responsive
element (ISGF-2) start point"
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100.0%; Pred. No. 2.2e-10;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                         "IFN-gamma-activated site (Fc gamma start point"
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                                                                                                                                                                                                                                                                                                                                                                                                           (BOEF ) BOEHRINGER MANNHEIM GMBH.
         /*tag= f
1475..1567
/*tag= g
/note= "exon 3"
1568..1774
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1175..1797
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/note= "exon 4"
1798..2324
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note= "exon 5"
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20-JUN-1995;
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Weiss

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Immunoregulatory protein leukocyte specific transcript-1 - whose prodn. in U937 cell lines is stimulated by interferon-gamma, useful for diagnosis and therapy, e.g. of tumours
                                                                                                                                                                                                                                                                                               Human genomic DNA (AAT45451) codes for a novel cytokine-like
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WPI; 1999-190035/16.
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06-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the human lipolysis stimulated receptor (LSR) genomic sequence. The novel LSR binds lipoproteins in presence of free fatty acids (FFA) and binds cytokines in absence of FFA. The nucleic acid and its fragments are used as probes and primers for detection and/or amplification of LSR genes; for production of recombinant LSR; for detecting allelic variants, mutations, deletions, loss of heterozygosity and genetic abnormalities in the gene. LSR, recombinant cells and transgenic animals are used to screen for chemical interacting with LSR,
                                                                                                                                                                                                                                                                                                                                                                                                                                  gctaatttttgtatttttttagtagagacggggtttcaccatgttggccaggatggtct 10548
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4279 GCTAATTTTTGTATTTTTTAGTAGAGGGGGTTTCACCATGTTGGCCAGGATGGTCT 4221
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
immunoregulatory protein (AAW07680), leukocyte specific transcript-1
                 (LST-1), which is characterised in that its prodn. in 1937 cell lines is stimulated by interferon-gamma by a factor of over 1000 and that it binds to the surface of leukocytes. The gene was obtd. from a human B-cell line CAH cosmid library by hybridization to a TNFA probe. Alternative splicing yields a 97-amino acid LST-1 isoform (AAM07681). An LST-1 cDNA clone (AAM45452) has also been isolated. LST-1 nucleic acids can be used for recombinant protein prodn., as probes, and in the gene therapy of e.g. tumours, esp. using methods based on homologous recombination.
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                                                                                                                                                                                                                                                             Sequence 5581 BP; 1410 A; 1441 C; 1542 G; 1188 T; 0 other;
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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nes 59; Conserv
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                             its recycling rate and/or specificity of receptor activity, particularly for reducing the level of leptin, lipoproteins, chylomicrons and/or triglycerides. The chemicals are thus useful for treating eating disorders, particularly obesity (and related diseases such as atheromatosis, atheroselerosis, hypertension and diabetes) or anorexia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9009 cccagttaattttttttttttagtagagatggggtttcaccatgttggccaggctggt 9067
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and leptin, are used to modulate the number of LSR in a
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 21721;
                                                                                                                                                                                                                                                                                                                       Sequence 21721 BP; 4980 A; 5688 C; 6170 G; 4865 T; 18 other;
                                                                                                                                                                                                                                                also disease associated with abnormal cytokine metabolism.
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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97FR-0010088.
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Gaps
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                                Length 23187;
                                 Query Match 0.2%; Score 59; DB 21; Length 23 Best Local Similarity 100.0%; Pred. No. 1.7e-10; Matches 59; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                               Human leptin fragment coding sequence SEQ ID NO: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..2000
/*tag= a
/note= "5' regulatory region"
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complement(1375..1393)
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complement(819..837)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(607..625)
                                                                                                                                                                                                                ВР
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1330..1373
/*tag= o
replace(1374,G)
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/*tag= m
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/*tag= d
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   delete(19040)
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... b
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1096..1115
/*tag= k
1224..1242
/*tag= 1
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1516..1534
/*tag= v
1602..1621
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799..817
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946..963
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/standard_name= "single nucleotide polymorphism"
/note= "marker 9-24-486 (A18)"
replace(15826,T)
                                                                                                                                                                                                                                                                                                                                                                      /frequency= 0.05
/standard_name= "single nucleotide polymorphism"
/note= "marker 9-9-246 (A23)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= ao
/standard_name= "single nucleotide polymorphism"
/note= "marker A'3"
replace(8394,G)
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//standard_name= "single nucleotide polymorphism"
/note= "marker A'9"
replace(11878,T)
/*tag= "/standard_name= "single nucleotide polymorphism"
/note= "marker A'10"
                                                                             /standard_name= "single nucleotide polymorphism"
/note= "marker 9-6-187 (A19)"
replace(19567,G)
                                                                                                                                          ffrequency= 0.35
/standard_name= "single nucleotide polymorphism"
/note= "marker 9-7-148 (A20)"
                                                                                                                                                                                                                           /frequency= 0.14
/standard_name= "single nucleotide polymorphism"
/note= "marker 9-7-325 (A21)"
                                                                                                                                                                                                                                                                                            /*tag= ai
/standard_name= "single nucleotide polymorphism"
/note= "marker 9-7-367 (A22)"
replace(20158,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= al
/standard_name= "single nucleotide polymorphism"
/note= "marker LSRX10-BM (A25)"
replace(606,T)
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/standard_name= "single nucleotide polymorphism"
/note= "marker A'1"
insert(5141,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= an
/standard_name= "single nucleotide polymorphism"
/note= "marker A'2"
insert(7428,C)
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/standard_name= "single nucleotide polymorphism"
/note= "marker A'6"
delete(9950..9957)
/note= "marker A'7"
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/*tandard_name= "single nucleotide polymorphism"
//note= "narker A'8"
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/standard_name= "single nucleotide polymorphism'
/note= "marker A'4"
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/note= "marker A'5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /frequency= 0.26
/note= "marker LSRX9-BM (17-1-240) (A24)"
replace(21108,G)
                                                                                                                                                                                                                                                                                                                                                                                                                         delete(20595..20597)
                                                /*tag= af
/frequency= 0.01
                                                                                                                                                                                              replace(19744,A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replace(10021, A)
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| complement(/429/44/) /*tag= bf 79958012 /****** | /*tag= bg 83757393 /*tag= bh | replace(8394,C) | /"Lag- D1 complement(83959413) /*tag= bi | complement(85768593) | 86858703 /*tag= bl | replace(8704,T) | complement(87058723) | 96 | /*tag= bo replace(9028,G) | /*tag= pp complement(90299047) | /*tag= bq 96229639 | /*tag= br 99319949 | /*tag= bs complement(99519969) | <u>~</u> | 9 | e(| /*tag= bw complement(99789996) | /*tag= bx 1000210020 /*tag= bx | replace(10021,G) | complement(1002210040) | Ψ. | 1049210512 /*tag= cc | complement(1054610563) /*tag= cd | 1185711877 /*tag= ce | complement(1099611015) /*tag= cf | e(11878,T) cg | complement(1187911897) /*tag= ch | 1197211990 /*tag= ci | 1200512023 /*tag= ci | 1216312282 /*tag= ck | u w | | 0.2%; Score 59; DB rity 100.0%; Pred. No. 1.7 | 1 |
|---|---|---|--|------------------------------|--|-------------------------|----------------------|--------------|-----------------------------------|-----------------------------------|-----------------------|------------------------------|-----------------------------------|---|-------------|-----------------------------------|------------------------------------|---------------------------------------|-------------------------|------------------------------|---|-------------------------|-------------------------------------|-----------------------------------|-------------------------------------|------------------------------|-------------------------------------|-------------------------|-----------------------------------|-------------------------|-----------------------------------|-----------------------|---|-----------------------|
| misc_binding primer_bind | misc_binding | allele | misc_binding | primer_bind | misc_binding | allele | misc_binding | misc_binding | allele | misc_binding | primer_bind | misc_binding | misc_binding | misc_binding | primer_bind | allele | misc_binding | misc_binding | allele | misc_binding | primer_bind | primer_bind | | | | | | primer_bind | primer_bind | exou | primer_bind | | Ouery Match 0.3 Best Local Similarity 100. Matches 59. Conservative | ב ה |
| 는 문 도 도 도 도 도 도 | - pa pa | , pag 12 | - paq 1E | | 1 1 | | | ped 1 | | pad 1 | PA | | see! | pad | - per H | | | | | | | FF. | FT | FT | FT | | | FT | | FT FT | FF | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| /"cay- w complement(16161635) /*tag- x 1769 1787 | 1,03.:1/8/ /*tag= y replace(1788.C) | /*tag= z /*tag= z complement(1789_1807) | /*tag aa aa 2001 | /*tag= ab /product= "LSR" | /hote= "this sequence contains introns" 20012356 | /*tag= ac /number= 1 | 2035 | 20622081 | /*tag= ae complement(20742093) | 20842102 | /*tag= ag 23722390 | /*tag= an replace(2391,C) | ž | /*Ldg= aj complement(25632580) /*+*^~ | ĕ | /"Lay="a1 complement(24832500) | /* Lag= all 34553474 /*t=or= | /:-cug- un 3540.;3884 /*†ac= ac | /number = 2 3759 377 | /*tag- /*tag- 37753792 | /*tag= aq /*tag= aq replace(3778.T) | _ | 'n | /*tag= at complement(43364356) | | /*tag= av replace(4498,G) | /*tag= aw complement(49024920) | /*tag= ax 49794997 | /*tag= ay complement(49995017) | | /*tag= ba complement(51425160) | /*tag- bb 66386655 | /*tag= bc complement(70727089) /*tag= bd | 7.cay- Da 74097427 |

ó ngatggggtttcaccatgttggccaggctggt 9067 re 59; DB 22; Length 23187; ed. No. 1.7e-10; Mismatches 0; Indels 0; Gaps .12436)

Leu codon"

ဌ

codon

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/*teg= a
/note= "specifically claimed region of intronless
cDNA identified by exon trapping"
           Adult onset polycystic kidney disease; APKD; autosomal dominant; mutant; transversion; transition; deletion; insertion; ds.
                                                                                                                                                                                                   /*tag= d
/note= "insertion, results in frameshift"
                                                                                                                                                                  /*tag= c
/note= "replaces Val codon by Leu codon"
                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated human polycystic kidney disease gene and its useful for treatment of polycystic kidney disease and
                                                                                                                                /*tag= b
/note= "changes Val codon
replace(50796..50797, cg)
                                                                                                                                                                                       insert(51827..51828,
                                                                 Location/Qualifiers
4379..5272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1; 65pp; English.
                                                                                                                                                                                                                                                                                                 95US-0381520.
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                                                                                                                                                                                                                                                                                                                                 (IGIG-) IG LAB INC.
(UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                   Connors TD,
                                                                                                                                                                                                                                                                                                                                                                              Oian F;
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-222017/22
                                                                           misc_feature
                                                                                                                                                      old_sequence
                                                                                                                                                                                       old_sequence
                                            Homo sapiens
                                                                                                                       old_sequence
                                                                                                                                                                                                                                 WO9612033-A1
                                                                                                                                                                                                                                                                             11-0CT-1995;
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12-OCT-1994;
                                                                                                                                                                                                                                                       25-APR-1996.
                                                                                                                                                                                                                                                                                                                                                                            Landes GM,
                                                                                                                                                                                                                                                                                                                                                                   Burn TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                              carriers
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                                                                  Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the human polycystic kidney disease 1 (PKD1) gene. The PKD1 gene or polypeptide may be used to treat autosomal dominant polycystic kidney disease (AFKD), and identify carriers of mutant PKD1 genes, i.e. subjects susceptible to AFKD. Antibodies (AD) that distinguish between normal and mutant PKD1 sequences can also be used in diagnostic tests. Anti-PKD1 AD may also be used to perform subcellular and histochemical localisation studies, and to block the function of PKD1. Ab are also useful in rational drug design studies to identify and test inhibitors of PKD1. Sense and antisense sequences derived from the PKD1 gene may
                                                                                                                                                                                                                                                                                                                                                                                     Human polycystic kidney disease gene, PKD1 - useful to treat and diagnose human autosomal or adult onset polycystic kidney disease
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                                                                                                                                                                                                                                                                                                                                   Klinger K;
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                                                                                                                                                      Human; polycystic kidney disease 1; PKD1; treatment; autosomal dominant polycystic kidney disease; APKD; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polycystic kidney disease normal PKD1 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.2%; Score 59;
100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Pages 90-118; 257pp; English.
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                                                                 BP
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                                                                 53526
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96US-0655360.
                                                                                                           (first entry)
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Best Local Similarity 100.C
Matches 59, Conservative
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                                                                 DNA;
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                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-018511/02.
                                                                AAT94101 standard;
                                                                                                                                Human PKD1 gene.
                                                                                                                                                                                                          W09744457-A1
                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                       22-MAY-1997;
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                                                                                     AAT94101;
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mutants -screening for

Klinger KW;

Germino G,

Dackowski W,

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The present sequence is that of the normal human PKD1 gene from chromosome 16. Mutations in this gene (e.g. transitions, transversions, deletions and/or insertions) are associated with a cadult-onset polycystic kidney disease (APKD). The PKD1 locus is adult-onset polycystic kidney disease (APKD). The PKD1 locus is CC-rich (62.4%). Comparison of this sequence with a previously reported partial cDNA sequence revealed differences at three locations (see features table). The most significant difference is the presence of two additional cytosine residues on the plus-strand at position 456 of the previously reported sequence. The insertion results in a frame-shift in the predicted protein coding sequence, cleading to replacement of 92 C-terminal amino acids with a novel. Is amino acid C-terminals. The PKD1 gene contains 23 Alu repeats.

There is a region consisting of 17 tandem copies of a perfect 27 bp repeat and two large CT-rich regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53577 BP; 8495 A; 17681 C; 15785 G; 11616 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 53577;
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Pred. No. 1.4e-10;
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100.0%; Pred. No. 1...
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Best Local Similarity 100.0
Matches 59; Conservative
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Page 35

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autoimmune disease; hepatic disease; renal disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID AAT72165 standard; cDNA to mRNA; 2688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δy
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  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiinflammatory; nootropic; neuroprotective; antiallergic; cancer; tumour; neurodegenerative disorder; developmental abnormality; allergy; foetal deficiency; blood disorder; immune system disorder; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                 Human PKD1 locus between chromosomal markers ATPL (ATP6C) and D16S84.
                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the human polycystic kidney disease 1 (PMD1) locus between chromosomal markers ATPL (ATPGC) and D16S84. The PMD1 gene or polypeptide may be used to treat autosomal before dominant polycystic kidney disease (APMD), and identify carriers of mutant PMD1 genes, i.e. subjects susceptible to APMD. Antibodies (Ab) that distinguish between normal and mutant PMD1 sequences can also be used in diagnostic tests. Anti-PMD1 Ab may also be used to perform subcellular and histochemical localisation studies, and to block the function of PMD1. Ab are also useful in rational drug design studies to identify and test inhibitors of PMD1. Sense and antisense sequences derived from the PMD1 gene may used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                              Human polycystic kidney disease gene, PKDI – useful to treat and diagnose human autosomal or adult onset polycystic kidney disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein encoding nucleotide sequence SEQ ID NO:79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 53577 BP; 8495 A; 17684 C; 15782 G; 11616 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.2%; Score 59; DB 19; Length 53577;
100.0%; Pred. No. 1.4e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                        Klinger
                                                                                                  autosomal dominant polycystic kidney disease; APKD; ss.
                                                                                        Human; polycystic kidney disease 1; PKD1; treatment;
                                                                                                                                                                                                                                                                         Germino G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                Example 5; Pages 60-89; 257pp; English.
                                                                                                                                                                                                                                                                        Dackowski W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ98085 standard; cDNA; 2191 BP
AAT94108 standard; DNA; 53577 BP
                                                                                                                                                                                                              96US-0658136
96US-0655360
                                                                                                                                                                                          97WO-US08799
                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection and therapy.
                                                                                                                                                                                                                                                (GENZ ) GENZYME CORP.
                                                                                                                                                                                                                                                                        Connors T,
                                                                                                                                                                                                                                                                                                         WPI; 1998-018511/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                           01-JUN-1998
                                                                                                                          Homo sapiens
                                                                                                                                                                                          22-MAY-1997;
                                                                                                                                                                                                              03-JUN-1996;
24-MAY-1996;
                                                                                                                                            W09744457-A1
                                                                                                                                                                    27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ98085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                       Burn T,
Qian F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ98085/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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The polynucleotide sequences given in AA298017 to AA298108 encode the human secreted proteins given in AAY87064 to AAX8723. Human secreted burners given in AAX87064 to AAX87223. Human secreted corporation can have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; immunosuppressive, antiinflammatory; nootropic; neuroprotective; and antiallergic. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new colynucleotides. Human secreted protein s and their polynucleotides can be used for developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, diseases of the immune system, autoimmune diseases, hopatic and renal diseases, inflammation, allergies, alzheimer's disease, behavioural disorders, schizophrenia, cardiovascular disorders, reproductive disorders, gastrointestinal cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders asthma, sepsis, and proteins are also used as food additives or proteins or polynucleotides can also be used as food additives or proteins are also useful for identifying their chied the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Alzheimer's disease; behavioural disorder; schizophrenia; osteoporosis; infection; AIDS; spinal cord injury; transplant rejection; diabetes; asthma; sepsis; acne; psoriasis; cardiovascular disorder; reproductive disorder; gastracintestinal disorder; respiratory disorder; metabolic disorder; food additive; preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shi Y;
Young PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes, useful for diagnosis and treatment of, cancers, neurological or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D, Rosen CA, Moore PA,
Brewer LA, Florence KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2191 BP; 597 A; 524 C; 503 G; 565 T; 2 other;
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5.7e-10;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Komatsoulis G, Dua..
Finer R, Olsen HS, Brew.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 353-354; 494pp; English.
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100.0%; Prev
0; N
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                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0092921.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-161128/14.
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Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY87132
                                                                                                                                                                                                                                         WO200004140-A1.
                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                           14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DW,
                                                                                                                                                                                                                                                                                                    27~JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 5-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mucenski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lafleur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT72165/c
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17358 tttttttgagacggagtttcactcttgttgcccaggctggagtgcaatggcgtgatct 17415

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/note- "Protein encoded by DNA from the human brain which has different expression from the normal protein when in an Alzheimer's disease patient"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= e
/note= "Protein encoded by DNA from the human brain which
has different expression from the normal protein
when in an Alzheimer's disease patient"
                                                                                                                                                                                                 /*tag= a
/note= "Protein encoded by DNA from the human brain which
                                                                                                                                                                                                                                                                          /*tag= b
/note= "Protein encoded by DNA from the human brain which
                                                                                                                                                                                                                              has different expression from the normal protein when in an Alzheimer's disease patient"
                                                                                                                                                                                                                                                                                                         has different expression from the normal protein when in an Alzheimer's disease patient"
                                                                                                                                                                                                                                                                                                                                                                                  has different expression from the normal protein when in an Alzheimer's disease patient"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a DNA fragment which is complementary the mRNA sequences whose level of expression in the brains of Alzheimer's disease patients varies from normal individuals. The present sequence represents a specifically claimed DNA fragment in which the expression is augmented to at least twice that in normal cases. The sequence, and antibodies to the proteins encoded by the sequence, may be used in the diagnosis, treatment and investigation of Alzheimer's disease.
                                                                                                       Human; brain; Alzheimer's disease; diagnosis; antibody; expression; ds
                                                                                                                                                                                                                                                                                                                                                                 /note= "Protein encoded by DNA from the human brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequences with varied expression in normal and Alzheimer patients – used for diagnosis and treatment of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW19931, AAW19932, AAW19933, AAW19934, AAW19935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2688 BP; 826 A; 456 C; 508 G; 898 T; 0 other;
                                                                         Alzheimer's disease DNA sequence from plasmid pGCS55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sakaki Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 27-31; 90pp; Japanese.
                                                                                                                                                                   location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kuga T, Nakagawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95JP-0322745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-JP03630
                                                                                                                                                                                                                                                                                                                                      1042..1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2370..2465
                                                                                                                                                                                                                                                                                                                                                                                                                 . 2272
                                           (first entry)
                                                                                                                                                                                                                                                            560..802
                                                                                                                                                                                    .489
                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
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                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9721807-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-DEC-1996;
                                           25-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hashida H,
            AAT72165;
                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                       CDS
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Human; biallelic marker; arachidonic acid metabolism; genotyping; detection; hybridisation; phenotype; haplotype; SNP; polymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; identification; ERBM; 12-LO-RBM; elcosonoid-related biallelic marker; 12-LO-related biallelic marker; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes polynucleotides including biallelic markers derived from genes involved in arachidonic acid metabolism and from genomic regions flanking those genes. Methods from the present invention may be used to select individuals for clinical trials and predict responses to treatment with drugs. The polynucleotides may be awed in hybridisation assays, sequencing assays and specific amplification assays for identifying an eicosanoid-related biallelic marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a segment of nucleotides containing an ERBM. The polynucleotides are useful in diagnostic kits. The markers may be used to detect conditions and genotypes associated with arachidonic acid metabolism. AAC57367 to AAC58018 and AAB24019 and AAB24020 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNPs) in the polynucleotide sequences from the present invention have been given as their corresponding degenerate bases e.g. a polymorphic base of C or T has been given as Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel biallelic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism -
Gaps
                                                                                                                                                                                                                         Arachidonic acid metabolism related genomic biallelic marker #651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oy 17383 igitgoccaggoiggagigoaaiggogigaictoagoicacigoaacoicogocico
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DD 14685 TGTTGCCCAGGCTGGAGTGCAATGGCGTGATCTCAGGCTCACTGCAACCTCCGCCTCCC
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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100.0%; Pred. No. 3.7e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 67; Page 790-796; 802pp; English.
                                                                                                           AAC58017 standard; DNA; 20674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0275267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0119917
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                                                                                                                                                                                      (first entry)
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58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                WO200047771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-FEB-1999;
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07-MAY-1999;
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                                                                                                                                                   AAC58017;
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Gaps

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Indels

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Length 2688;

0.2%; Score 58; DB 18; 100.0%; Pred. No. 5.5e-10;

Query Match 0.2 Best Local Similarity 100. Matches 58; Conservative

; Pred. No. 5.5 0; Mismatches

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RESULT 40
AAC98168
                                  intron
                                                                                                                                                      5'UTR
                                                                                                                                                                                                                                                                            3'UTR
                                                                                     exon
                                                                                                                                                                                                         CDS
Human; glycosyl sulfotransferase-4; GST-4; immunosuppressive; therapy; selectin binding inhibitor; gene therapy; inflammation; systemic lupus exythematosus; SLE; rheumatoid arthritis; diabetes; polyarteritis nodosa; polymyositis; systemic sclerosis; dermatitis; glomerulonephritis; myasthenia gravis; Sjogren's syndrome; adrenalitis; Hashimoto's disease; Grave's disease; hypoparathyroidism; anaemia; demyelinating disease; cirrhosis; ulcerative colitis; allergic rhinitis; myocarditis; adult respiratory distress syndrome; eczema; psoriasis; asthma; hypersensitivity; rheumatic fever; tissue rejection; chromosome 16q23.1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number= 5
/note= "Includes 17 base pairs of 5'UTR, the ORF
and all of 3'UTR"
47939..47955
/*tag= j
/note= "Dortion of 5' untranslated region (5'UTR)"
47956..49128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product= "Human glycosyl transferase-4alpha
                                                                                                                                                      Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.
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15593..35674
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7939..49746
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6634..46700
                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
32847..32922
                                               AAD02697 standard; DNA; 160552 BP.
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83348..96412
/*+=_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= 4a_5U3
35675..45093
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /number= 3
/label= 4a_5U2
45186..46633
/*tag= f
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46701..47938
/*tag= h
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32923..35592
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49129..49746
/*tag= 1
83257..83347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'number= 2
                                                                                                                  (first entry)
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/number= 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'number=
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                  02-MAY-2001
                                                                                 AAD02697;
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                              AAD02697
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The present sequence is human glycosyl sulfotransferase-4 (GST-4) genomic DNA encoding GST-4alpha and GST-4beta. GST-4 gene is found on chromosome 16q23.1.

Chromosome 16q23.1.

Chromosome 16q23.1.

GST is a type 2 membrane protein useful for inhibiting a binding event between a selectin and a selectin ligand, which comprises contacting the selectin with a non-sulphated selectin ligand, GST and a small molecular generation in inhibiting a selectin mediated binding event. GST is also useful in inhibiting a selectin mediated binding event. GST is useful in gene therapy to treat disorders such as acute or chronic inflammation, systemic lupus erythematosus (SLE), rheumatoid arthitis, polyarteritis nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes, glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Habhimoto's disease, Grave's disease, adrenalitis, hypoparathyroidism, pernicious caneemia, demyelinating diseases, cirrhosis, ulcerative colitis, contactory distress syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis, accompaniation as pronchial asthma, hypersensitivity, rheumatic fever and tissue rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                        /*tag= r
objection of 5' untranslated region (5'UTR)"
98474..9661
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                                                                                                                                                         /*tag= q
/note= "Includes 17 base pairs of 5'UTR, the ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
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/product= "Human glycosyl transferase-4beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                           /cons_splice= (5'site:NO, 3'site:NO)
98457..99968
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100.0%; Pred. No. 2.4e-10;
tive 0; Mismatches 0;
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                                                                                                                                                                                                   and all of 3'UTR"
98457.98473
/*tag= r
/label= 4a_501
96485..98456
/*tag= p
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (GST-4beta)"
99662..99968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-138471/14.
P-PSDB; AAY72639, AAY72640.
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Best Local Similarity 100.(
Matches 58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200106015-A1
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(first entry)

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Polynucleotide library used to determine cancerous states of mammalian
                                         Human colon cancer cell line polynucleotide sequence SEQ ID NO:1847.
                                                                      Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; so.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 689; 1097pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           Williams LT, Escobedo
Reinhard C, Giese K,
Lamson G, Drmanac R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-126369/11.
                                                                                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON CORI
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Leshkowitz D,
                                                                                                                                               Homo sapiens.
                                                                                                                                                                          W09958675-A2
                                                                                                                                                                                                                                   13-MAY-1999;
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27-0CT-1998;
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                                                                                                                                                                                                                                                                             5-MAY-1998
                                                                                                                                                                                                                                                                                           15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells
  AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB5324 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                            identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
                                                                                                                 detection;
                                                                                     Human colon cancer antigen nucleotide sequence SEQ ID NO:178.
                                                                                                                 cancer antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 740 BP; 186 A; 163 C; 190 G; 198 T; 3 other;
                                                                                                                                                                                                    infectious disease; cardiovascular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 603-604; 2104pp; English.
AAC98168 standard; cDNA; 740 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders such as colon cancer
                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                    08-MAR-2000; 2000WO-US05883.
                                                                                                                                                                                                                                                                                                                                                 99US-0124270.
                                                                                                                 cancer; colon
                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAB53411.
                                                                                                                                                                                                                                                           WO200055351-A1.
                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                 colon
                                                                                                                                                                                                                                                                                                                                                 12-MAR-1999;
                                                       09-MAR-2001
                                                                                                                                                                                                                                                                                         21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
                          AAC98168;
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C, Pot D, Kassam A; n M, Drmanac S, Labat I; Stache-Crain B;

Kennedy GC, P R, Dickson M, Garcia PD,

Randazzo F, Kennedy G Crkvenjakov R, Dickso Garcia V, Jones LW,

Kita D,

Innis MA,

98US-0085696. 98US-0105234. 98US-0105877.

CORP.

99WO-US10602 98US-0085426 98US-0085537 Sudduth-Klinger J;

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                                                                                         genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can be used in diagnosis for detecting and mapping related genes. They can be used as probes for detecting and dispeases and disorders (e.g. identification of
AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
libraries constructed from human colon cancer cell lines. The present
invention also describes a method of detecting differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                    pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-negative breast cancer, oung cancer, and colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy 17556 aggottggtctcgaactcctgacctcaggtgatccacccacctcagcctcccaaagtg 17612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            532
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Pred. No. 1.5e-09;
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100.0%; Pred. No. 1.5e-
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Best Local Similarity 100.7
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Gaps

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Length 740; Indels

1.5e-09;

0.2%; Score J,, 100.0%; Pred. No. 1.5e-n+ive 0; Mismatches

Query Match 0.2° Best Local Similarity 100. Matches 57; Conservative

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g

Score 57; DB 21;

AAA01856 standard; cDNA; 788

RESULT 41 AAA01856/c AAA01856;

XX

Lander ES;

Ireland JS,

AAC72064;

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The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to disease of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single nucleotide polymorphism; SNP; human; genetic disease; disease susceptibility; cardiovascular system; endocrine system; neurological system; forensic testing; paternity testing; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.2%; Score 57; DB 21;
100.0%; Pred. No. 1.5e-09;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                              , Daley GQ,
Sklar P;
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                                                                                                                                             30-MAR-2000; 2000WO-US08440
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Best Local Similarity 100.0
Matches 57; Conservative
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                                                                                                                                                                                                                                                                                            Cargill M,
Patil N, S
                                                                                                                                                                                                                                                      AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-611722/58.
                                                           WO200058519-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200058519-A2
                                                                                                                                                                                                                                                                                              Altshuler D,
Lipshutz RJ,
                      Homo sapiens.
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                                                                                                                                                                                      31-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or G.
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                                                                                                                    Single nucleotide polymorphism; SNP; human; genetic disease; disease susceptibility; cardiovascular system; endocrine system; neurological system; forensic testing; paternity testing; ds.
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100.0%; Pred. No. 1.5e-09;
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                                                                             Single nucleotide polymorphism containing sequence #631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Daley GQ, Ireland JS,
Sklar P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          medicine and genetic analysis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 5; 214pp; English.
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                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                       (WHED ) WHITEHEAD INST (AFFY-) AFFYMETRIX INC.
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                                                                                                                                                                                                                                                  WO200058519-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Altshuler D,
Lipshutz RJ,
                                                                                                                                                                                                          Homo sapiens,
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The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
                Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing,
                                                                                                                                                                                                                                diseases. Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or G.
                                                                                                                                                                                                                                                                                                      Sequence 792 BP; 213 A; 195 C; 145 G; 238 T; 1 other;
                                                                                       Claim 1; Fig 5; 214pp; English
                                                           medicine and genetic analysis
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Best Local Similarity 100.
Matches 57; Conservative
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Patil N, S
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Lipshutz RJ,
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                                                                                                                                          Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis
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1.5e-09;
hes 0;
                                                                        Ireland JS,
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100.0%; Pred. No. 1.5
ive 0; Mismatches
                          (WHED ) WHITEHEAD INST BIOMEDICAL RES
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Sklar P;
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 99US-0127248.
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Best Local Similarity 100.(
Matches 57; Conservative
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Patil N, S
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Patil N, S
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                                          AFFYMETRIX INC
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31-MAR-1999;
                                                                     Altshuler D,
Lipshutz RJ,
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Lipshutz RJ,
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                                          (AFFY-)
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                                                                                                                      4644
                                                                                                                                                 213 ccaggctggagtgcagtggcatgatctcggctcactgcaacctccacctcctgggtt 269
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                   Length 792;
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             Score 57; DB 21;
Pred. No. 1.5e-09;
0.2%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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Sklar P;
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nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to disease of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
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                                                                                                                                                      Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or {\rm G}.
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Sklar P;
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                                                                                                                                                                                                                                    Sequence 792 BP; 213 A; 195 C; 145 G; 238 T; 1 other;
                                                                                                                                                                                                                                                                                          0.2%; Score 57; DB 21; 100.0%; Pred. No. 1.5e-09; iive 0; Mismatches 0;
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Patil N, S
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of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or {\rm G}.
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                                                                                          Sequence 792 BP; 212 A; 195 C; 145 G; 239 T; 1 other;
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0; Mismatches
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                                                                                                                                                                                 Score 57;
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Patil N, Sklar P;
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Best Local Similarity 100.C
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Matches 57; Conservative
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Lipshutz RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC72115;
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Gaps

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Indels

0; Mismatches

Note: The degenerate codon within the sequence represents the position

diseases

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Gaps

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Indels

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Conservative

57;

Matches

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Chibraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of prognosis of diseases and disorders (e.g. identification of responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J, Innis MA, Garcia PD, Sudduth-Klinger J;
Randazzo F, Kennedy GC, Pot D, Kassam A;
Crkvenjakov R, Dickson M, Drmanac S, Labat I;
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide library used to determine cancerous states of mammalian
Human colon cancer cell line polynucleotide sequence SEQ ID NO:1846
                                                                                                                                                                                                                                                          Human; colon cancer; tumour; diagnosis; gene expression product; probb; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 801 BP; 207 A; 204 C; 202 G; 178 T; 10 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 689; 1097pp; English.
                                                                                                                        BP.
                                                                                                                      AAA01855 standard; cDNA; 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0085537.
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98US-0105877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escobedo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glese K,
Drmanac R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-126369/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams LT,
                                                                                                                                                                                                                                                                                                                                                                                W09958675-A2.
                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-1998;
15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-0CT-1998;
27-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reinhard C,
Lamson G, I
                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1998
                                                                                                                                                        AAA01855;
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4588
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                                                                                                                                                                                                    Hypoxia induced gene; HIG; cancer; ischaemia; diagnosis; reperfusion; retinopathy; neonatal distress; pre-eclampsia; cardiac arrest; stroke; stress; hypoxia; ionising radiation; hypothermia; heat shock; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated hypoxia-inducible genes, used to develop products for diagnosis and treatment of hypoxia-related conditions, e.g. cancer, ischaemia, reperfusion, retinopathy, neonatal distress, pre-eclampsia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17556 aggottggtctcgaactcctgacctcaggtgatccacccacctcagcctcccaaagtg 17612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1466 BP; 345 A; 357 C; 392 G; 372 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.2%; Score 57; DB 20; I
100.0%; Pred. No. 1.3e-09;
ive 0; Mismatches 0;
                                                                                                                                                                            Human hypoxia induced gene HIG2 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (STRD ) UNIV LELAND STANFORD JUNIOR. (STRI ) SRI INT.
                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                              BP.
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/product= "HIG2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 2; 109pp; English.
                                                                                 AAZ25133/c
ID AAZ25133 standard; cDNA; 1466
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                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiac arrest or stroke
                                                                                                                                                                                                                                                                                                 274..465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giaccia AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-580418/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY42135.
                                                                                                                                                                                                                                                                                                                                                        WO9948916-A2
                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-1998;
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                 13-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Denko NC,
                                                                                                                       AAZ25133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koong AC;
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Best Local 9
 17556
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51

RESULT

Length 801;

Score 57; DB 21; I Pred. No. 1.5e-09;

0.2%; 8

Query Match Best Local Similarity

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The invention provides a method of inducing a prophylactic immune response to a self-antigen in a subject. The method comprises administering the antigen or its derivative or administering educated immune effector cells able to recognize and lyze cells expressing the self-antigen or its derivative. The method is used to stimulate an immune response against a self-antigen especially one expressed in a cancer or melanoma. The present sequence represents the DNA sequence encoding
                  Immune response; self-antigen; immune effector cell; cancer; melanoma; human; melanoma antigen; MART1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12671 gttggtcaggctggtctcaaactcctgacctcaggtgatctgcccgcctcagcctcc 12727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MART1; melanocyte differentiation antigen; melanoma; human; antigen presentation; adoptive immunotherapy; cancer; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human MART1 melanocyte differentiation antigen coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1559;
                                                                                                                                                                                                                                                                                                                                                                                      Method of inducing an immune reaction to a self-antigen by administering the antigen, especially useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1559 BP; 470 A; 330 C; 324 G; 435 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.2%; Score 57; DB 20; I 100.0%; Pred. No. 1.3e-09; rative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 3A-B; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human melanoma antigen hMART1.
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ID AA220065 standard; DNA; 1559
                                                                                                                                                                                     99WO-US06034.
                                                                                                                                                                                                                       98US-0078890.
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Best Local Similarity 100.(
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54..410
/*tag=
                                                                                                                                                                                                                                                             (GENZ ) GENZYME CORP
                                                                                                                                                                                                                                                                                                                                   WPI; 1999-580277/49.
                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY42634
                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                               Nicolette CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                             WO9946988-A1
                                                                                                                                                                                                                         20-MAR-1998;
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                                                                                                                                                                                   19-MAR-1999;
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                                                                                                                                                 23-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                              melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The nucleic acid encodes a melanoma antigen (MART-1) which is recognized by T-1ymphocytes. It is used for recombinant protein production, preferably using a baculo virus vector for expression in insect cell cultures. MART-1 protein is a source of immunogenic peptides (see AAR84196 for peptide M9-2) which are optionally modified (see AAR84180) and used in medicaments for the treatment or prevention (by immunization) of melanoma. Antibodies against MART-1 and its immunogenic peptides may be used in the detection and its immunogenic peptides may be used in the detection and isolation of MART-1 from a sample, the detection of which is indicative of a disease state (melanoma or metastatic melanoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding melanoma antigens recognised by T-lymphocytes - a vectors, host cells and antibodies, used to detect, treat and immunise animal against melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57; DB 16; Length 1559;
                                                                                                                                                               MART-1; melanoma antigen recognised by T-cells; melanoma; metastatic melanoma; tumour-associated antigen; immunogen; diagnosis; prognosis; prophylaxis; therapy; vaccine; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human melanoma antigen hMART1 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 115-116; 184pp; English.
                                                                                                                                                                                                                                                                          Location/Qualifiers
54..410
/*tag= a
                  AAT02714 standard; cDNA; 1559 BP
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94US-0231565
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                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawakami Y, Rosenberg SA;
                                                                                                                            MART-1 melanoma antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAR84212.
                                                                                          20-APR-1996
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                                                                                                                                                                                                                                          Mammalian
                                                      AAT02714;
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AAT02714
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Brooks-Wilson AR, Pimstone SN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200102568-A2.
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02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2001
             Hayden MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF65529;
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAF65529/c
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                                                                                                                                                                     This nucleotide sequence comprises a coding region for human spacifically recognised by HLA-A restricted tunnour-infiltrating specifically recognised by HLA-A restricted tunnour-infiltrating lymphocytes of melanome patients. The invention provides methods gainst an antigen in a patient. Genetically modified antigen presenting cells (APC) that are more potent presenters of exogenous peptide than the parental antigen-presenting cells are used. These APCs lack an effective endogenous TAPP (transporter associated with antigen processing) activity and present exogenous antigen on the major histocompatibility complex class I (MHC-I) antigen. Suitable exogenous antigens include a tunnour antigen, such as a minimal essential epitopeo of MARTI, which can complex with MHC-I. The genetically modified APCs are useful for inducing an immune response (claimed) against an antigen in a patient (adoptive immunotherapy), especially as vaccines against cancer in mammals, preferably humans. The cells are also useful for expanding in mammals, preferably culls, preferably cytotoxic I would a constitution of immune effector cells, preferably cytotoxic I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oy 12671 gttggtcaggctggtctcaaactcctgacctcaggtgatctgccggcctcagcctcc
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 57; DB 20; Length 1559;
Pred. No. 1.3e-09;
                                                                                                                 Preparing cells for use as cancer vaccines and in adoptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1559 BP; 470 A; 331 C; 323 G; 435 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 0.2%; Score 57; DB 1 Similarity 100.0%; Pred. No. 1.3 57; Conservative 0; Mismatches
                                                                                                                                                    Disclosure; Page 50-51; 55pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0151977.
2000US-0526193.
2000US-0213958.
            98US-0078880.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ABC1 genomic DNA
                                                          Kaplan
                                   (GENZ ) GENZYME CORP
                                                                              WPI; 1999-590956/50.
P-PSDB; AAY31980.
                                                                                                                                                                                                                                                                                                                                                                                         lymphocyte cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200115676-A2
                                                        Nicolette CA,
                                                                                                                             immunotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-1999;
15-MAR-2000;
23-JUN-2000;
          20-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF92831;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABCl expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
                                                                                                                 Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal trighyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klinger J, Kassam
nson G, Drmanac R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytostatic; gene therapy; colon cancer; prostate cancer; breast cancer; lung cancer; cancer detection; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 183999;
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edy GC, Pot D, Lamson G, Drm
kson M, Labat I, Leshkowitiz
Strache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.2%; Score 57; DB 22; Length 18
100.0%; Pred. No. 5e-10;
Live 0; Mismatches 0; Indels
   SM;
Clee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Innis MA,
Kennedy GC,
Dickson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF65529 standard; cDNA; 314 BP
                                                                                                                                                                                                                                                                       Claim 8; Fig 1; 317pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0142310.
99US-0142311.
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Reinhard C, Randazzo F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                        WPI; 2001-244356/25.
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Length 11967;

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which are tumour suppressor genes in human neuroblastoma. The genes are tumour suppressor genes, base sequence data of which are applicable as tumour suppressor genes, in studying mechanism of tumour body formation, and gene diagnosis of tumours as well as in developing anti-cancer drugs. AAP97787 to AAP9795 represent PCR primers used in the exemplification of the present invention, and AAP97830 to AAP97874 represent sequences given in the exemplification of the present
                                                                                                                                                                                        Sequence 11967 BP; 2877 A; 2760 C; 2873 G; 3457 T; 0 other;
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JAN-1995;
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                                                                                                                                                                                                                                                                                          55;
                                                                                                                                                    invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maley F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT71699;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:77.
                                    The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a homozygosity deletion domain co-existing in the 36-position of the first chromosome short arm (1p36) in human neuroblastoma. Also described are base sequences from the 1p36 position of human neuroblastoma cell lines (NB-1 and MASS-NB-SCH-1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human 1p36 homozygosity deletion domain from the 36-position of first chromosome short arm in human neuroblastoma cell lines, applicable e.g. in gene diagnosis of tumors as well as in developing anti-cancer drugs
                                                                                                                                                                                                                                                                                     antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 1; 1p36; neuroblastoma cell line; NB-1; anticancer; suppressor; human 1p36 homozygosity deletion domain; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 314 BP; 95 A; 66 C; 81 G; 71 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; I
                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. nc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56;
Pred. No.
Claim 9; Page 728; 1046pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF97863 standard; DNA; 11967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200116311-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakagawara A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF97863;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes the human deoxycytidylate (dCMP) deaminase intron 2, which comprises 20303 base pairs from nuclectides 1964-22266 of the dCMP deaminase sense strand. The dCMP deaminase gene contains a 5' untranslated region (including the promoter), 5 exons, 4 introns and a 3' untranslated region (including the stop signals). The gene can be used to produce recombinant dCMP deaminase, which can be used to convert dCMP to alloy, the dCMP gene can be altered (removed or mutated) to alter DNA replication in cells, which may lead
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                          Qy 17396 ggagtgcaatggcgtgatctcagctcactgcaacctccgcctcccgggttcaagc 17450
                                                                                                                                        8878 ggagtgcaatggcgtgatctcagctcactgcaacctccgcctcccgggttcaagc 8932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9013 gttaatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt 9067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding human deoxycytidylate deaminase - for production of recombinant deaminase
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                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human deoxycytidylate deaminase intron 2 encoding DNA.
DB 22; L
3.9e-09;
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ilarity 100.0%; Pred. No. 3.5e-09
Conservative 0; Mismatches 0
0.2%; Score 55; DB 100.0%; Pred. No. 3.9
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Column 83-100; 58pp; English.
                                                                                                                                                                                                                                                                                               AAT71699 standard; DNA; 20303 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant deaminase; dCMP; ds
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                                                       Conservative
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Best Local Similarity
Matches 55; Conserv
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The present invention describes a method for screening drug candidates.

The method comprises adding a drug to a cell that expresses an expression profile gene encoding a protein encoded by 5 sequences of defined base pairs as given in C55638. C55642, C55644 and C55653 or a sequence represented by Genbank accession number x92521, x62466, J04130, x62087 and x776534 (or a fragment) and determining the effect of the drug on the expression of the expression profile gene. An inhibitor of matrix metalloproteinase 19 (MMP-19), preferably an intibody, is useful for treating destructive macrophage disorders (DMD) by inhibiting DM development in a cell of an individual having arthitis. Antibodies to MMP-19 are useful for localising a therapeutic moiety preferably cytotoxic agent or a radioisotope to colorectal cancer tissue. A composition comprising MMP-19 is useful for eliciting an immune response in an individual. C55635 to C55710 represent human configuration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening drug candidates comprises adding a drug to a cell expressing an expression profile gene and determining the effect of the drug on the expression of the expression profile gene \,
deaminase gene, which contains a 5' untranslated region (including the promoter), 5 exons, 4 introns and a 3' untranslated region (including the stop signals). The gene can be used to produce recombinant dCMP deaminase, which can be used to convert dCMP to dUMP. Also, the dCMP gene can be altered (removed or mutated) to alter DNA
                                                                                                                                                                                                                                          Human; differentially regulated gene; macrophage development; diagnosis; matrix metalloproteinase 19; MMP19; antiarthritic; antiinflammatory; destructive macrophage development inhibitor; arthritis; colorectal cancer; immune response; ss.
                                                                                                                                                                     Length 26764;
                                                                                                                    Sequence 26764 BP; 7079 A; 5521 C; 6539 G; 7625 T; 0 other;
                                                                                                                                                                                                          0; Indels
                                                                                  replication in cells, which may lead to mutagenesis.
                                                                                                                                                                       DB 18; L
3.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human differentially regulated gene from Fig 36.
                                                                                                                                                             0.2%; Sco. 100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                BP.
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ID AAC55670 standard; cDNA; 245
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                                                                                                                                                                                                          Conservative
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                                                                                                                                                                       Query Match
Best Local Similarity
Matches 55; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                              AAC55670;
                                                                                                                                                                                                                                                                                                                               RESULT
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   555555588
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                                                                                                                                                                                                                                                                                                                                                                                                  untranslated region, including promotor"
 6385 gttaatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt 6439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding human deoxycytidylate deaminase - for production of recombinant deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes the human deoxycytidylate (dCMP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number= 5
25468..26764
/rag= k
/note= "3' untranslated region"
                                                                                                                                                                                         Human deoxycytidylate deaminase gene.
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                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..1317
                                                                                      BP,
                                                                                                                                                                                                                          Recombinant deaminase; dCMP; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weiner KXB
                                                                                  AAT71696 standard; DNA; 26764
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22384..23740
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23741..23837
/*tag= h
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*tag= f
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3838..25391
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**taq= e
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/note= "5'
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1426..1827
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/*tag= d
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                                                                                                                                                                                                                                                                                                          misc_feature
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                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                       20-AUG-1997
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RESULT

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                                                                                                                                                                                                                                                                                                               Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     upstream regulatory sequences and to design expression and secretion
                                                            ;
 Length 245;
                                Indels
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0.2%; Score 54; DB 21; 11 100.0%; Pred. No. 1.8e-08; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Giordano J;
                                                                                                                                                                                                                                                                              Human secreted protein 5' EST, SEQ ID NO: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 356; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duclert A,
                                                                                                                                                                                 BP
                                                                                                                                                                               AAC00358 standard; cDNA; 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2000; 2000EP-0200610.
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P-PSDB; AAG00352.
               Similarity
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                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                               54;
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 Query Match
                  Local
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                             Matches
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The invention identifies regions of the human factor IX (iFRIX) gene, and a region of the human protein C (APF54018) are age-related capulatory sequences. The hFIX age-related regulatory sequences are designated AES' (AAF54018) and are found in the 5' (AFF54018) and are found in the 5' (AFF54018) and are found in the 5' UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 2164-2165 of AAF54018). These elements act synergistically to crease hFIX levels over the lifespan of an individual; however, they can independently exert effects on hFIX mRNA in an age-related manner, with AES' acting to stabilise hFIX mRNA, and AE3' acting to increase hFIX mRNA is and AE3' acting to increase hFIX mRNA is and contains two PEA-3 (polyoma virus activator 3) elements of AAF64081), and contains two PEA-3 (polyoma virus activator 3) elements of companies and contains two PEA-3 (polyoma virus activator 3) elements of 5'-GAGGAA-3' and 5'-CAGGAAG-3'. The age-related regulatory sequences of the invention, along with their homologues, variants and fragments, may be used in the construction of recombinant expression vectors for the expression of a desired sequence in an age-related fashion in a host cell. Preferred target genes for expression in such age-regulatable constructs and conductor of the pro-coaquants factor IX and factor VIII, and the anti-coagulants protein and reporter proteins such as luciferase. Preferred promoters factor IX promoter, the T7 promoter, the T3 promoter and the SPG promoter. The expression vectors include the human factor IX promoter, the T7 promoter coagulation (e.g., the pro-coaquants factor IX promoter, the T3 promoter and the SPG promoters of secondariants are seed in the treatment of sense, diabetes, Alzheimer's disease, the treatment of thrombosis, cardiovascular disease, diabetes, Alzheimer's disease, cancer, osteoporosis, osteoarthritis and dementia. Specifically, they may be used to expression or transgenic cells or animals age-related rise in factor IX ansequic cells and animature age-re
                                                                                                                                                                                                        Age-related gene regulation; specific; gene expression; human factor IX; hFTX; AE3'; 3' UTR; 3' untranslated region; AE3': element; age-regulatable expression construct; antisense therapy; gene therapy; thrombosis; cardiovascular disease; diabetes; Alzheimer's disease; Parkinson's disease; cancer; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to nucleic acid sequences which regulate gene expression in an age-related manner and/or in a liver-specific manner. The invention identifies regions of the human factor IX (hFIX) gene, and
                                                                                                                                                                hFIX gene AE3' age-related regulatory region fragment, SEQ ID NO:59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New regulatory elements that control age-related gene expression, useful in gene therapy and for reducing Factor IX expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 177; 225pp; English
                      DNA; 723 BP.
                                                                                                                                                                                                                                                                                                                                      osteoarthritis; dementia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0328925.
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                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kurachi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-061708/07
                      AAF54060 standard;
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                 30-MAR-2001
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                                                                   AAF54060;
AAF54060/
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Gaps

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0.2%; Score 54; DB 21; Length 354; 100.0%; Pred. No. 1.6e-08; Ive 0; Mismatches 0; Indels

Conservative

Local Similarity

Query Match

54;

Best Loca Matches Qy 17555 caggetggtetegaaetectgaeeteaggtgatecaeceaecteageetecea 17608
 Db 265 caggetggtetegaaetectgaeeteaggtgatecaeceaecteageetecea 318

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression in an age-related manner and/or in a liver-specific manner. The invention identifies regions of the human factor IX (hFIX) gene, a region of the human factor IX (hFIX) gene, and regulatory sequences. The hFIX age-related regulatory sequences are designated AE5' (AAF4016) and AE3' (AAF54017) and are found in the 5' UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 2164-2165 of AAF54018) and are found in the 5' UTR (at position 1264-2165 of AAF54018) and 3' UTR (at position 2164-2165 of AAF54018) respectively. These elements act synergistically to increase hFIX levels over the lifespan of an individual; however, they with AE5' acting to stabilise hFIX mRNA, and AE3' acting to increase hFIX mRNA levels, over time. AE5' also directs liver-specific expression. The HC gene age-related regulatory sequence is found in the 5' UTR (AAF54081), and contains two PED-3 (polyoma virus activator 3) elements 5'-GAGGAAA-3' and 5'-CAGGAAG-3'. The age-related regulatory sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Age-related gene regulation; liver-specific; gene expression; numan factor IX; hFIX; ARE<sup>5</sup>, Age regulatable expression construct; antisense therapy; gene therapy; thrombosis; cardiovascular disease; diabetes; Algheimer's disease; Parkinson's disease; cancer; osteoporosis;
that contain vectors of the invention are useful as models of these diseases, in screening for potential therapeutic agents and for studying normal processes such as ageing and gene expression. Fragments and homologues of age-related regulatory sequences, are useful as probes to detect, isolate or identify other such sequences in samples. The present sequence represents an AB3' region fragment.
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to nucleic acid sequences which regulate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB60281, AAB60282, AAB60283, AAB60284, AAB60285, AAB60286,
AAB60287, AAB60288, AAB60289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New regulatory elements that control age-related gene expression, useful in gene therapy and for reducing Factor IX expression
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0
                                                                                                                                                                                                           Length 723;
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                                                                                                                                               Sequence 723 BP; 213 A; 147 C; 179 G; 184 T; 0 other;
                                                                                                                                                                                                                               1.4e-08;
                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                       0.2%; Score 54; DB
ilarity 100.0%; Pred. No. 1.4
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human factor IX (hFIX) gene, SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 8A-E; 225pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF54018 standard; DNA; 38059 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteoarthritis; dementia; ds
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Best Local Similarity
Matches 54; Conserv
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the invention, along with their homologues, variants and fragments, may be used in the construction of recombinant expression vectors for the expression of a desired sequence in an age-related fashion in a host call. Preferred target genes for expression in such age-regulatable expression vectors include those encoding proteins involved in blood anti-coagulants protein C and antithrombin III) human factor VIII, and the alpha-l-antitrypsin, PEA-3 protein and reporter proteins such as culfierse. Preferred promoters for use in such age-regulatable expression vectors include the human factor IX promoter, the T7 promoter, the T3 promoter and the SP6 promoter. The expression vectors of the invention may be used in gene therapy to provide age-related and/or liver-specific expression of target genes. Age-regulatable constructs may be used in gene therapy to provide age-related and/or liver-specifically, they may be used to such age-related conditions such as thrombosis, cardiovascular disease, diabetes, Alzheimer's disease, parkinson's disease, cancer, osteoporosis, osteoarthritis and dementia. Specifically, they may be used to express factor IX antisense mRNA in the treatment of thrombotic conditions associated with the natural age-related rise in factor IX expression. Transgenic cells or animals that contain vectors of the invention are useful as models of these contains a general and gene expression. Fragments and centers and detect, isolate or identify other such sequences, are useful as probes to detect, isolate or identify expression. Fragments in samples. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD 31675 CCCAGTTAATTTTGTATTTTAGTAGAGGTTTCACCATGTTGGCCAGG 31622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 38059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38059 BP; 12326 A; 7397 C; 7441 G; 10895 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9009 cccagttaatttttgtatttttagtagagatggggtttcaccatgttggccagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.2%; Score 54; DB 22; I
100.0%; Pred. No. 6.5e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT25953 standard; cDNA to mRNA; 72 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents the hFIX gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene signature HUMGS08188.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
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Local S.m.
54; C
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                                                              A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7817 "CS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA ibraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(") as the sole primer. Since the 3'-en untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs on 1901A+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tag (5' EST) for
to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26414 tccgagacttaacgaaaatagtatttcagctgcaataaagattgagtttgcaa 26466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.2%; Score 53; DB 16; I
100.0%; Pred. No. 4.8e-08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 72 BP; 25 A; 10 C; 16 G; 20 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein 5' EST, SEQ ID NO: 34149.
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Claim 1; Page 1967; 2245pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy; chromosome mapping; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC30074 standard; cDNA; 192 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5' EST;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1033401-A2
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derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length CDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                               9015 taatttttgtattttagtagagatggggtttcaccatgttggccaggctggt 9067
                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                          Length 192;
                                                                                                                                                                                                                                                                                   Human gene expression product cDNA sequence SEQ ID NO:1395.
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                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard
Stache-Cran B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crkvenjakov R, Dickson M, Drmanac S;
                                                                                                                                         Sequence 192 BP; 31 A; 48 C; 45 G; 65 T; 3 other;
                                                                                                                                                                                                            3.9e-08;
                                                                                                                                                                                            0.2%; Score 53; DB 21;
                                                                                                                                                                                                     100.0%; Prea. ...
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                                                                                                         expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                      BP,
                                                                                                                                                                                                                                                                                                                                                                                   AAZ13926 standard; cDNA; 300
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98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US01619
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                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-494092/41.
                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-APR-1998;
28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo saptens
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mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polymucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polymucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polymucleotides of the invention are especially used in the dilanguage and management of colorectal cancer, breast cancer, and lung cancer. The polymucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                                                                         peptide analogues and antagonists.
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Sequence 300 BP; 79 A; 72 C; 81 G; 68 T; 0 other;

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                    Gaps
                                .;
0
    Length 300;
                   Indels
            3.6e-08;
    Score 53; DB 20;
Pred. No. 3.6e-08
0.2%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
                   Conservative
           Similarity
                  53;
    Query Match
             Local
           Best Loc
Matches
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prostate cancer;
                                                       cancer; cancer detection; ss.
                                                 gene therapy; colon cancer;
                                       Novel human polynucleotide, SEQ ID NO: 1282
          BP.
     526/c
AAF65526 standard; cDNA; 350
                                                                                              30-JUN-2000; 2000WO-US18374.
                             (first entry)
                                                      breast cancer; lung
                                                  cytostatic;
                                                                          WO200102568-A2.
                                                                 Homo sapiens.
                             09-APR-2001
                                                                                     11-JAN-2001
                   AAF65526;
                                                  Human;
     AAF65526/
RESULT
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Klinger J, Kassam mson G, Drmanac R; Leshkowitiz D; Lamson G, LT, Escobedo J, Innis MA, Garcia PD, C, Randazzo F, Kennedy GC, Pot D, Li OV R, Drmanac S, Dickson M, Labat I, Garcia V, Jones LW, Strache-Crain B; (CHIR) CHIRON CORP. (HYSE-) HYSEQ INC. Williams LT, Reinhard C, Crkenjakov Kita D, Ga

99US-0142310. 99US-0142311.

02-JUL-1999; 02-JUL-1999; À;

WPI; 2001-091805/10.

a Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -

Claim 9; Page 727; 1046pp; English.

The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and

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mmson G, Drmanac R;
                                                                               compositions to
            (e.g.
                                                                                                                                                                                                                                         Gaps
their gene products are used as genetic or biochemical markers (e.g. blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polymorlocations, polypeptides and antibodies against them can be used in pharmaceutical compositions treat the cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytostatic; gene therapy; colon cancer; prostate cancer; breast cancer; lung cancer; cancer detection; ss.
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Leshkowitiz D;
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                                                                                                                                                                                                                                                                                          Length 350;
                                                                                                                                                                                                                                                                        9015 taatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt
                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                  Sequence 350 BP; 103 A; 71 C; 98 G; 77 T; 1 other;
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:zo F, Kennedy GC, Pot D, La
mac S, Dickson M, Labat I,
Jones LW, Strache-Crain B;
                                                                                                                                                                                                     Score 53; DB 22; I
Pred. No. 3.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human polynucleotide, SEQ ID NO: 1283.
                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                   0.25,
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                              AAF65527 standard; cDNA; 352
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99US-0142311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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, Drmanac S,
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-091805/10.
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Kita D, Garcia V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200102568-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-1999;
02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-2001
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                                                                                                                                                                                                                                         53;
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antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective;
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The invention relates to 53 novel genes and their fragments (nucleic acid sequences: AAX79011-X79064; amino acid sequences AAX1411-Y14464) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated human genes and the secreted polypeptides they encode
ureat tne cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia.
                                                                                                                                                                           ;
0
                                                                                                              Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       r R, Ferrie AM, Florence C;
Olsen HS, Rosen CA, Ruben SM;
                                                                                                                                              0; Indels
                                                              79 T; 0 other;
                                                                                                          0.2%; Score 53; DB 22;
100.0%; Pred. No. 3.5e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein gene 40 clone HFIUR10.
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                                                              Sequence 352 BP; 103 A; 72 C; 98
                                                                                                                                                                                                                                                                                             AAX79050 standard; DNA; 541 BP.
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970S-0061463.
970S-0061527.
970S-0061529.
970S-0061532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US21142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ebner
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                            53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Greene JM,
Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-277587/23.
                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duan R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY14450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Florence KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9919339-A1
                                                                                                                                                                                                                                                                                                                                                          17-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-0CT-1997
09-0CT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Young PE,
                                                                                                                                                                                                                                                                                                                           AAX79050;
                                                                                                                                                                                                                                                             9
                                                                                                                                            Matches
                                                                                                                                                                                                                                                                            AAX79050,
                                                                                                                                                                                                                                                             RESULT
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polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 53 polynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; mouse; chicken; rat; secreted expressed sequence tag; sEST; expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antidiammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiulcer; osteopathic; neuroprotective; notroportective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (SESTs), isolated from human, mouse, chicken and rat tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; hemostatic; thrombolytic; antilnflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polynucleotides, and encoded proteins, comprising secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                        9067
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                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                                        9015 taatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                               484 TAATTTTTGTATTTTTAGTAGAGATGGGGTTTTCACCATGTTGGCCAGGCTGGT
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                                                                                                                                                                               Sequence 541 BP; 109 A; 170 C; 149 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted expressed sequence tag SEQ ID NO:781.
                                                                                                                                                                                                                                                                                DB 20; L 3.2e-08;
                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                0.2%; Score 53; 100.0%; Pred. No.
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Bowman MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 407; 803pp; English.
                                                                                                           (see AAX79011 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA44206 standard; cDNA; 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US24206.
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                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCCOY JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-317938/27
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200021991-A1
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Merberg D,
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New isolated human polynucleotides

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anticorvulsant, and antidepressant. The sESTS can be used for gene identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the sESTS. Proteins encoded by the sESTS met useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease, tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45916 to AAA45911 represent linker variants which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer; human; colon; breast; lung; transmembrane receptor; Arpase; integral membrane protein; aspartyl protease; GATA family; wnt family; transcription factor; G-protein alpha subunit; protein phosphatase; phorbolester binding protein; diacylglycerol binding protein; trypsin; protein kinase; tyrosine phosphatase; developmental signalling protein; protein; protein; genetic mapping; diagnostic; detection; treatment; cervical; melanoma; colorectal adenocarcinoma; wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma; leukemia; lymphoma; dysplasia; hyperplasia; endometrium; adrenal;
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                           0.2%; Score 53; DB 21; Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones LW, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                      3.1e-08;
nes 0; Indels
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se K, Innis MA;
                                                                                                                                                                                                                                                                                                 Sequence 651 BP; 141 A; 150 C; 140 G; 219 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human validated cancer cell derived cDNA #332.
                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. 3.1 ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX99010 standard; cDNA; 746 BP.
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98US-0105877
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Best Local Similarity 100.C
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9933982-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-1998;
21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 70
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by screening for differential expression in colon cancer, breast cancer and lung cancer cell lines. The polynucleotides of the invention are represented in AAX98175-X99118 and encode polypeptides of protein cancer cell lines. The polynucleotides of the invention are represented in AAX98175-X99118 and encode polypeptides of protein cancer families selected from 4 transmembrane segments integral membrane proteins, 7 transmembrane receptors, ATPases associated with various cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of transcription factors, G-protein alpha subunit, phorbolesters or dacy1glycerol binding proteins, protein subunit, phorbolesters or dacy1glycerol binding proteins and ww/rsp5/www fomain containing proteins. The encoded polypeptides also have a functional domain selected from Ank repeat, basic region plus leucine zipper transcription factors, bromodomain. E-hand, SH3 domain, WD domain/G-beta repeats, zinc finger (CZH2 type), zinc finger (CCHC class), and zinc-binding metalloprotease domain. The polynucleotides encode polypeptides with similarity to known protein families and are predicted to have similar properties. The novel polynucleotides can be used to develop products for use as therapeutic appinglactions. In particular, the product can be used for the detection and management of cancers. They can be used for the detection and management of cancers. They can be used for the detection and management of cancers. They can be used for the detection and management of cancers. They can be used for the detection and management of cancers. They can be used for the detection and management of cancers. They can be used for the detection and management of cancers. They can be used for the detection and management of cancers. They can be used for the detection and management of cancers. They can be used for the detection and management of cancers. They can be used for the detection and management, and lymphomas such as highlicocytic lawkemia, and hymphomas and congenital alvenda and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
prostate or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of
                                                                                                                                    novel isolated human polynucleotides obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; food additive; preservative; chromosome identification; cancer; female reproductive system disorder; immune disorder; wound healing; cardiovascular disorder; neurological disease; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9015 taatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt 9067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.2%; Score 53; DB 20; Length 746;
100.0%; Pred. No. 3e-08;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 746 BP; 200 A; 151 C; 185 G; 185 T; 25 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein gene 45 SEQ ID NO:55.
                                                                             Claim 1; Page 546; 591pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC74381 standard; cDNA; 788 BP
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                                                                                                                                       This invention describes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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WO200058340-A2.

05-OCT-2000.

WPI; 1999-430243/36.

infection; ss Homo sapiens.

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14-APR-2000; 2000WO-JP02455.
                 26-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human secreted proteins given in AAB39402 to AAB39451. Corrections and proteins have activities based on the tissues invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Example of activities include: Correction; immunosuppressive; nootropic; neuroprotective; antitiviral; antiallergic; hepatotropic; antidiabetic; antifungal; antiparasitic; antiallergic; hepatotropic; antidiabetic; antimoranty; antitioral; culherary; anticonvulsant; antidiabetic; antifungal; antiparasitic; and cardiant. The polypuclectides and polypeptides are useful for preventing, treating or ameliorating a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capablities. The polypucledide are useful for chromosome identification. They are also useful as probes for diagnosing a disorder related to the female reproductive system, particularly breast and/or ovary cancer. They are also useful in the gene therapy of breast cand ovarian cancer. Secreted protein nucleic acids, proteins, controductions and antagonists are useful in the diagnosis, creatment and prevention of: (a) cancer; (b) immune disorders; (c) cardiovascular disorders; (d) wound healing; (e) neurological diseases; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. AAC74318 to AAC74316 and AAB39401 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                               Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                           The polynucleotide sequences given in AAC74337 to AAC74386 encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; histidine domain-protein tyrosine phosphatase; HD-PTP;
chromosome 3p21.3; gene deletion; tumour suppressor; cytostatic;
lung cancer; tumour; gene therapy; diagnosis; recombinant production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9015 taattittgtattittagtagagatggggtttcaccatgttggccaggctggt 9067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tyrosine phosphatase HD-PTP gene exon 2, SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.2%; Score 53; DB 21; Length 788; 100.0%; Pred. No. 38-08; 1.1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 788 BP; 196 A; 174 C; 224 G; 194 T; 0 other;
                                                                                                       Komatsoulis G;
                                                                                                                                                                                                                                             Claim 1; Page 353; 391pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC81263/c
ID AAC81263 standard; DNA; 1024
                                                                          (HUMA-) HUMAN GENOME SCI INC
23-MAR-2000; 2000WO-US07724.
                            26-MAR-1999; 99US-0126510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53; Conservative
                                                                                                       Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                     WPI; 2000-594638/56.
                                                                                                                                                  P-PSDB; AAB39446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anticancer; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200063392-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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use in cancer diagnosis and investigation. HD-PTP proteins, nucleic acids and antibodies may be used in the treatment, investigation and diagnosis of cancers, particularly those of the lung. The present sequence represents exon 2 of the human HD-PTP gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel human tyrosine phosphatase, histidine domain-protein tyrosine phosphatase (HD-PTP, AAB29661) and to human HD-PTP nucleic acids (AAC81224, AAC81225, AAC81263). The HD-PTP gene is located on chromosome 3p21.3. This region is frequently found to be deleted in lung cancers, and is therefore thought to contain a tumour suppressor gene. The invention also relates to expression vectors and host cells containing human HD-PTP nucleic acids; the recombinant production of HD-PTP, anticancer drugs containing HD-PTP; gene therapy compositions containing DNA encoding HD-PTP; diagnostic reagents containing HD-PTP outleic acids and an immunoassay method using HD-PTP-specific for HD-PTP; and an immunoassay method using HD-PTP-specific antibodies for HD-PTP; and an immunoassay method using HD-PTP-specific antibodies for HD-PTP; and an immunoassay method using HD-PTP-specific antibodies for HD-PTP; and an immunoassay method using HD-PTP-specific antibodies for HD-PTP; and an immunoassay method using HD-PTP-specific antibodies for HD-PTP; and an immunoassay method using HD-PTP-precipic antibodies for HD-PTP; and an immunoassay method using HD-PTP-precipic antibodies for HD-PTP; and an immunoassay method using HD-PTP-precipic antibodies for HD-PTP; and an immunoassay method using HD-PTP-precipic antibodies for HD-PTP.
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                                                                                                                                                                                                                                                                                                                                                  Human tyrosine phosphatase with oncostatic activity encoded by a gene frequently deleted in lung cancer, useful for treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1024 BP; 241 A; 234 C; 287 G; 262 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.2%; Score 53; DB 21; I
100.0%; Pred. No. 2.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding a human transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 129-130; 134pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                         (KYOW ) KYOWA HAKKO KOGYO KK
99JP-0108842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
276..440
/*tag= b
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                                                                                                                                                                                                                                    WPI; 2000-672740/65
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Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                            P-PSDB; AAB29666
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16-APR-1999;
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                                                                                                                                                      Shimizu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                       of tumors
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Hayashi K;

Sugiyama T,

us-09-434-382-28.oli.rng

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Isogai T, Nishikawa T, Kawai Y,
                                WPI; 2001-093989/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC88096;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
           Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC88096/
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                                                                                                                                                                                                                                                       Agonists and antagonists of the protein are protein prosent sequence another and antagonists of the protein are used to treat a disease or condition associated with overexpression of the protein. Diseases and conditions which can be treated include cell proliferative.

Immunological, reproductive, smooth muscle and neurological disorders e.g. arteriosclerosis, myeloma, leukaemia, acquired immunodeficiency syndrome (AIDS), allergies, ovulatory defects, angina, hypertension, stroke, Alzheimer's disease, epilepsy and Tourette's disorder. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues where protein expression may be correlated with disease e.g. to determine absence, presence or excess expression of HTMP or to monitor regulation of HTMP expression during therapeutic intervention.
                                                                                                             Baughn MR;
                                                                                                                                                                           New human transmembrane proteins are used to treat a disease or condition associated with decreased expression of functional HTMP e.g. Tourette's disorder, angina and leukaemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                 The present sequence encodes a human transmembrane proteins (HTMP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA encoding a membrane or secretory protein clone PSEC0127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; membrane protein; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9015 taatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt 9067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.2%; Score 53; DB 21; Length 1721; Best Local Similarity 100.0%; Pred. No. 2.5e-08; Matches 53; Conservative 0; Mismatches 0; Indels (
                                                                                                             Reddy R, Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1721 BP; 306 A; 579 C; 503 G; 333 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                             Tang YT, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secretory protein; membrane
rheumatoid arthritis; diabetes; ss.
                                                                                                                                                                                                                         Claim 4; Page 116; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF93811 standard; cDNA; 1773 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0194179.
2000JP-0118775.
2000JP-0183766.
                                                                                                                      Yang J;
                               22-MAR-2000; 2000WO-US07817
                                                    99US-0125537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUL-2000; 2000EP-0114090
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                                                                                       (INCY-) INCYTE PHARM INC.
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                                                                                                                                              WPI; 2000-579485/54.
                                                                                                                        Azimzai Y,
                                                                                                                                                          P-PSDB; AAB18972
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11-JAN-2000;
02-MAY-2000;
                                                      22-MAR-1999;
16-JUN-1999;
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                                                                                                             La l
          28-SEP-2000
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                                                                                                                         DAM,
                                                                                                            Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 74
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This invention relates to nucleic acid sequences AAF93744 - AAF93916
which encode human secretory or membrane proteins represented by
AAB88131 - AAB8819. Included in the invention are primers
CAAF893917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
CDNA sequences of the invention. The invention also includes methods for
the production of antibodies directed against the proteins, and cDNA
sequences, which can be used in vaccines. The polynucleotide sequences
can be used in gene therapy. The polynucleotide sequences and the
sequences which can be used in the prevention, treatment and
diagnosis of diseases associated with inappropriate secretory
protein/membrane protein expression. The nucleic acids and complementary
companies also be used as DNA probes in diagnostic assays
companies and their neactions (PCR) to detect and quantitate the
presence of similar nucleic acid sequences in samples. They may also be
used to study the expression and function of secretory proteins/membrane
polypeptides and their role in metabolism. The polypeptides may be used
as antigens in the production of antibodies against them and in assays to
dentify modulators (agonists and antagonists) of expression and
activity. The antibodies and antagonists may also be used as therapeutic
agents to down regulate expression and activity. The antibodies may also
be used as diagnostic agents for detecting the presence of the
polypeptides; in samples (e.g. by enzyme linked immunosorbant assay
contribits, and diabetes.
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                                                                                 Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; FLEXHT; full-length molecules expressed in human tissue; diagnosis; gene expression; genetic linkage; genetic variability; antianaemic; anticonvulsant; antiarteriosclerotic; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1773 BP; 489 A; 384 C; 417 G; 483 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB 22;
Pred. No. 2.5e-08;
                                                                                                                                                                                                            Claim 1; SEQ ID 135; 609pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. nc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ulcerative colitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
P-PSDB; AAB88384
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Rasool

Oscier D,

Liu Y,

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This sequence represents DNA originating from human leukaemia associated gene 1 (Leu1). The invention relates to B-cell chronic lymphocytic leukaemia (B-CLL) associated nucleic acids, including the present sequence, and amino acids. In humans, the Leul and Leu2 genes (see AAX58797 and AAX58801) have been identified as adjacent in B-CLL patients. Leul and Leu2 are strong candidate tumour suppressor genes involved in B-CLL leukaemogenesis. B-CLL associated nucleic acids can be used in gene thrarpy and for the production of proteins, which are used for the development of drugs against leukaemia and other malignancies of the same genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2127 BP; 665 A; 332 C; 466 G; 664 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                    Chronic lymphocytic leukemia nucleotides and proteins
                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Page 75-76; 81pp; English.
                                                                                                                                                                                                                   (KARO-) KAROLINSKA INNOVATIONS AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  area, for raising antibodies, and
                                                                                                                                                                           97SE-0004162.
                                                                                                                                      98WO-SE02052
1416..1426
/*tag= a
                                                                                                                                                                                                                                                       Grander D,
                                                                                                                                                                                                                                                                                                             WPI; 1999-337986/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 53; Conserv
                                                                                                                                                                           13-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09947540-A1
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                                                                                                27-MAY-1999
                                                                                                                                                                                                                                                                         Zabarovsky
                                                                                                                                                                                                                                                       Einhorn S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ24899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
      unsure
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Matches
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    ö
                                                                                                                                                                                                                                                                                                                                                                                                                        AAC88070 to AAC88124 encode the 55 FLEXHT (full-length molecules expressed in human tissues) proteins given in AAB36579 to AAB36633. The present invention describes an isolated polypeptide (A) comprising an amino acid sequence selected from one of 55 amino acid sequences 42-876 residues in length, corresponding to FLEXHT-1 to FLEXHT-55, a 90 % identical sequence, and a biologically active or immunogenic fragment of the sequence. The FLEXHT proteins can have antianeamic, anticonvulsant, antiarteriosclerotic, immunomodulatory, cytostatic, antiasthmatic, antilnflammatory, hepatotropic, antidiabetic, antisout, antillocr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and antirheumatic activities, and can be used in gene therapy. The polynuclectide sequences can be used to express the protein sequences. Pharmaceutical compositions comprising FLEXHT can be used to treat diseases or conditions associated with altered expression of functional FLEXHT. The proteins and polynucleotides can be used to diagnose and treat disorders including anaemia, epilepsy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atherosclerosis, developmental disorders, cancers, and immunological disorders such as asthma, bronchitis, cirrhosis, Crohn's disease, diabetes mellitus, gout, Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis, psorlasis, rheumatcid arthritis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                 Baughn MR, Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                Human FLEXHT protein and DNA sequences, useful for treating immunological disorders, developmental disorders, and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 53; DB 22; Length 1991;
Pred. No. 2.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9015 taatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chronic lymphocytic leukaemia; tumour suppressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1991 BP; 604 A; 485 C; 452 G; 450 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leul gene; leukaemia-associated gene 1; human; B-CLL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human leukaemia-associated gene 1 (Leu1) cDNA.
                                                                                                                                                                                                               Batra S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.2%; Scor.
100.0%; Pred. No. 2...
0; Mismatches
                                                                                                                                                                                                                                   Shih LL;
                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 152-153; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                 Reddy R,
                                                                                                                                                                                                                                   Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX58811 standard; cDNA; 2127 BP
                                                                                            99US-0311894.
99US-0311937.
99US-0311940.
                                                        12-MAY-2000; 2000WO-US13299.
                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53; Conservative
                                                                                                                                                                                                                 Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                     WPI; 2001-016234/02.
P-PSDB; AAB36605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                   Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ulcerative colitis
                                                                                                                                                                                                                 Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                              14-MAY-1999;
                                                                                                              14-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-AUG-1999
                    23-NOV-2000
                                                                                                                                                                                                                                   Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX58811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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in diagnostic kits.

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                                                               Gaps
                                                                                                                                                                     ö
Length 2127;
                                                                                                                                   9015 taatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt
                                                                   Indels
0.2%; Score 53; DB 20; I
100.0%; Pred. No. 2.4e-08;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein gene 89 clone HUFAK67.
                                                                                                                                                                                                                                                                                                                                                              AAZ24899 standard; DNA; 2596 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                   Conservative
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respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;

pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;

24-MAR-2000; 2000WO-US08020.

WO200062736-A2 Homo sapiens.

cancer; ss.

26-OCT-2000

99US-0127958 EAST CAROLINA. J W.

06-APR-1999;

(UYEC-) UNIV (NYCE/) NYCE

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secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin protein as compared to the numen protein only.

The invention (e.g. AA224802) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AA224811-224907; amino acid sequences AAX41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypoptides in sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 95 polynocleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                               New isolated human genes, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                             Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a nucleic acid molecule which encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                            Rosen CA, Yu G, Young PE, Feng P, Soppe
N, Duan RD, Kyaw H, Ebner R, Lafleur DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.2%; Score 53; DB 20; Length 2596; 100.0%; Pred. No. 2.3e-08; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2596 BP; 790 A; 433 C; 500 G; 873 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 350-351; 484pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (see AAZ24811 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF21203 standard; DNA; 5996
                                       980S-0078573
980S-0078574
980S-0078574
980S-0078577
980S-0078578
980S-0078579
980S-0078579
                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                98US-0080314.
                                                                                                                                                                                                                                                                        Shi Y, Moore PA;
            98US-0078563
98US-0078566
                                                                                                                                                                  98US-0080313
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Best Local Similarity 100.0
Matches 53; Conservative
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Endress GA,
                                                                                                                                                                                                                                                                                                      WPI; 1999-562050/47.
                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY41396
                                                                      19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
                                        19-MAR-1998;
19-MAR-1998;
                                                                                                                                                                              01-APR-1998;
                                                                                                                                                  01-APR-1998
                                                                                                                                     19-MAR-1998
                                                                                                                    19-MAR-1998
                                                                                                                                                                  01-APR-1998
                                                                                                                                                                                                                                                             Wei Y, En
Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                               disorders
                                                                                                                                                                                                                                          Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF21203;
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Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -

WPI; 2000-679539/66.

Nyce JW;

present invention describes low adenosine (A) content antisense

Disclosure; Page 1117-1118; 1592pp; English.

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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analysesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and malignancies, such as stimulating and activating peptide factors and malignancies, such as stimulating and activating produced specific and non-specific enzymes, chemokines, andogenously produced specific and non-specific enzymes, chemokines redeptors, adenosine receptors, bradykinin receptors, central nervous system (DNS) and peripheral nervous and non-nervous system proteins, adenosine receptors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CP), allergie rhinitis (AN), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and artisone olivonucleotides may be used in that expensent human polynucleotide frammants and expensed in the expersent humans of the expensed in the experient condition and expense of informal expensed in the expense or expensed in the expense of information rejection, bulmonary insertions and artisones of information is expensed in the expense or expense or information is and expense or inform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9067
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100.0%; Pred. No. 2e-08;
tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9015 taatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 79
AAA35081/c
ID AAA35081 standard; DNA; 6056 BP.
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Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human low adenosine antisense oligonucleotide related sequence #2770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
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Gaps

1138 TAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGT 1086

BP

AAC91210 standard; DNA; 7720

80

RESULT

g

AAC91210

AAC91210;

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The present invention describes a new composition comprising an antisense oligonuclectide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antinflammatory, antiallergies, and/or inflammation. The ON can have antinflammatory, antiallergies, and/or inflammation. The ON can have antinflammatory, antiallergies, and/or caseful for the treatment of diseases associated with inflammation, impediated airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, pain, cystic isthmosis, pulmonary hypertension, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPP), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including chreat and prostate cancer. The reduction of the adenosine content of the ONS reduction of the odenosine secretors causing release of deoxyadenosine which activates adenosine receptors causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bronchoconstriction and inflammation. AAA32313 to AAA33312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA3392) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences
                                                                                                                                                                                       phosphorothioate; impaired respiration; infilammation; allergy; allergy; disease; bronchoconstriction; inhibitor; antinfilammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma: respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                  adenosine receptor; low adenosine antisense oliqonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                   Human adenosine receptor related polynucleotide SEQ ID NO:2770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6056 BP; 1769 A; 1287 C; 1583 G; 1417 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 1038-1040; 1343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    given in the sequence listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US17712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0095212.
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                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-205971/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                WO200009525-A2
                                                                   28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-FEB-2000
                      AAA35081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nyce JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancers
                                                                                                                                                                  Human;
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The present invention provides a novel method of estimating the susceptibility of an individual to a developmental disorder using genetic and environmental variables. The method can be used in the diagnosis, prevention and treatment of disorders such as schizophrenia, spina bifida cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders, attention deficit disorder, obsessive compulsive disorder, chronic
                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing a developmental disorder, e.g. schizophrenia, by forming datasets (DS) of genetic (e.g. genotypes of folate metabolism alleles) and environmental variables affecting an individual and then comparing
                                                                                                 Human; schizophrenia; developmental disorder; spina bifida cystica; Tourette's syndrome; bipolar illness; autism; conduct disorder; attention deficit disorder; obsessive compulsive disorder; chronic multiple tic syndrome; learning disorder; polymorphism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple tic syndrome and learning disorders such as dyslexia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 7720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7720 BP; 1869 A; 1923 C; 1992 G; 1936 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacterial artificial chromosome (BAC)-F2 contig 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                          (UYNE+) UNIV NEW JERSEY MEDICINE & DENTISTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                       Human folate receptor I gene SEQ ID NO: 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 119-121; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 100.0%; Pi
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV83943 standard; DNA; 11811
                                                                                                                                                                                                                                                                                             99US-0318448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.2%;
                                                                                                                                                                                                                                                                  24-MAY-2000; 2000WO-US14354
                                                                                                                                                                                                                                                                                                                                                                                                                                                           these DS with reference DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                        Stenroos
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-025174/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                        WO200071754-A1
                                                                                                                                                                                                                                                                                              25-MAY-1999;
                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAR-1999
                                            20-MAR-2001
                                                                                                                                                                                                                                     30-NOV-2000
                                                                                                                                                                                                                                                                                                                                                       Johnson WG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV83943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV83943,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXX
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Gaps

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Yeast artificial chromosome; YAC; probe; eukaryotic chromosome;
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Gaps

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Length 6056;

0.2%; Score 53; DB 21; Length 60 100.0%; Pred. No. 2e-08; tive 0; Mismatches 0; Indels

53; Conservative

Similarity

Local

Matches

Query Match

9015 taatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt 9067

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contig, and exemplifies the invention. The specification describes nucleic acid sequence treation from a eukaryotic chromosome, including a nucleic acid sequences derived from a eukaryotic chromosome, including a necentromere or its functional derivative or hybrid, that are able, in a compatible cell, of replicating, acting as extra-chromosomal element and segregating during cell division. The sequences can be used to construct artificial chromosomes for use in gene therapy comprising a replicable, segregating nucleic acid that confers a specific phenotype on cells. Human artificial chromosomes can propagate in human cells and carry large amounts of DNA (e.g. therapeutic genes), and, being are also useful for generation of transgenic plants and animals, in production of proteins and to make diagnostic reagents, e.g. for expression of cytokines, receptors and growth factors, or to increase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a bacterial artificial chromosome (BAC)
                     cell division; artificial chromosome; gene therapy; BAC; transgenic; human artificial chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid comprising neocentromere sequences from eukaryotic chromosome - used to produce replicable, segregating artificial chromosomes that can carry large amounts of DNA for gene
neocentromere; replication; extra-chromosomal element; segregation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the copy number of a gene in a cell. The constructs may also be used for functional and structural analysis of chromosomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11811 BP; 3014 A; 2459 C; 2433 G; 3905 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 195-203; 540pp; English.
                                                                                                                                                                                                                                                                                                                      (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                             97AU-0006784.
                                                                                                                                                                                                           98WO-AU00352.
                                                                                                                                                                                                                                                       97AU-0008791.
                                                                                                                                                                                                                                                                                                                                                                Choo K,
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-009773/01.
                                                                                                                                                                                                                                                                                                                                                              Cancilla MR,
                                                                                                                                                                                                                                                                             13-MAY-1997;
                                                                                                                            WO9851790-A1
                                                                                                                                                                                                                                                       26-AUG-1997;
                                                                                                                                                                      19-NOV-1998
                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy
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treating, e.g. tumours - useful for, e.g. promoting coagulation in pro:thrombotic and tumour-associated vasculature, used with, e.g.

Disclosure; Page 185-193; 225pp; English.

factor 7 or anti-cancer agent

Composition containing coagulation-defective tissue factor for

98WO-US01012.

20-JAN-1998;

23-JUL-1998.

Homo sapiens. WO9831394-A2 97US-0035920. 97US-0036205.

22-JAN-1997; 27-JAN-1997;

27-MAR-1997

97US-0042427

King SW, Thorpe PE;

Gao B,

WPI; 1998-413821/35.

P-PSDB; AAW69613

(TEXA) UNIV TEXAS SYSTEM.

A composition has been developed which comprises at least 1 coagulationCaficient tissue factor (TF) compound that is modified to increase its
Caficient tissue factor (TF) compound that is modified to increase its
Calological half-life, but excluding modification that involves attachment
to an antibody (or its antigen-binding region) that binds to a component
cells, vasculature or stroma) of tumours. Also described in the present
invention are compositions containing any coagulation-deficient TF for
promoting coagulation. The coagulation-deficient TFs are used to promote
coagulation preferentially in prothrombotic vessels, particularly those
associated with: (i) benign growths (e.g. benign prostatic hypertrophy);
Calo induce tumour necrosis), or (iii) other disorders that involve
angiogenesis, e.g. diabetic retinopathy, restenosis, neovascular
cangiogenesis, e.g. diabetic retinopathy, restenosis, neovascular
candinistered sytemically, particularly intravenously, typically at
administered sytemically in tumour-associated blood vessels after systemic

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                                                                                                                                                                         Gaps
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                                                                                                                                                                 0.2%; Score 53; DB 20; Length 11811;
                                                                                                                                                                        Indels
                                                                                                                                                                     1.7e-08;
hes 0;
                                                                                                                                                                     100.0%; Pred. No. 1.7 ive 0; Mismatches
                                                                                                                                                                                                      AAV40401 standard; DNA; 13865 BP
                                                                                                                                                                 Query Match 0.29
Best Local Similarity 100.
Matches 53; Conservative
                                                                                                                                                                                                RESULT 82
                                                                                                                                                                                                    AAV40401/
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Human, truncated, tissue factor; tTF; TF; tumour; coagulation; blood vessel; Factor VIIa; FVIIa; benign growth; vascularised; benign prostatic hypertrophy; malignant; necrosis; angiogenesis; diabetic retinopathy; restenosis; neovascular glaucoma; psoriasis; rheumatoid arthritis; ss.

Human tissue factor full length genomic DNA sequence.

16-OCT-1998 (first entry)

AAV40401;

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Human; coding sequence polymorphism; vascular pathology gene; polymorphic site; phenotype correlation; forensic; paternity testing; medicine; genetic analysis; vascular disease; ds.
                                       Gaps
                                                                       9015 taatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt 9067
                                                                                           8526 TAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGT 8474
                                       ;
0
0.2%; Score 53; DB 19; Length 13865; 100.0%; Pred. No. 1.7e-08; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                               Human cholesteryl ester transfer nucleotide sequence.
                                                                                                                                                                                             AAZ32165 standard; cDNA; 13865
                                                                                                                                                                                                                                                                 (first entry)
                                       53; Conservative
                     Similarity
                                                                                                                                                                                                                                                               13-JAN-2000
                                                                                                                                                                                                                             AAZ32165;
       Query Match
                         Best Local
                                                                                                                                                             RESULT 83
AAZ32165/c
                                       Matches
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response

administration, even though they contain no targeting agent. They cause little if any injury to normal tissue; may produce a synergistic response when used with other antitumour agents and they eliminate the multi-step, and expensive, preparation of antibody-based targeting constructs. The

present sequence encodes human TF, from the present invention.

Sequence 13865 BP; 3711 A; 2955 C; 3240 G; 3959 T; 0 other;

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/*tag= h
/note= "Ambiguity base 'R' corresponds to 'A' in allele-1
and 'G' in allele-2 of biallelic marker 99-430-352"
complement (9495..9513)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the partial genomic DNA of human TBC-1 gene, comprising the 5' regulatory region, exons 1, Ibis and 2. TBC-1 gene is mapped to a candidate region of prostate cancer on chromosome 4. Single nuclectide polymorphism (SNP) is located within the biallelic marker region 99-430-352, localised in intron 1 of TBC-1 genomic DNA. TBC-1 gene is involved in the regulation of cell cycle and tissue differentiation in mammals. An alteration of TBC-1 sequence may be associated with a pathological condition, resulting in abnormal cell proliferation leading to cancer, e.g. prostate cancer. The biallelic markers can be used for generation of genetic maps, linkage analysis and association studies. TBC-1 sequence can be used for detection, diagnosis, genotyping, production of transgenic animals and screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human TBC-1 nucleic acids, useful for developing products
                                                                                                                                                                                                                                                                  note= "Detection of Biallelic marker 99-430-352"
                                                                                                                                                                           'bound_moiety= "Primer D1"
note= "Microsequencing of marker 99-430-352"
                                                                                                                                                                                                                                                                                                                                                                                                            /note="Microsequencing of marker 99-430-352" complement (9828..9845)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for the diagnosis and treatment of disorders involving cell
proliferation, particularly prostate cancer
                                                                                                       /bound_moiety= "Primer B1"
/note= "Amplification of amplicon 99-430"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Amplification of amplicon 99-430"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /bound_moiety= "Primer C1"
                                                                                                                                                                                                                                                                                                                                                                                             /bound_moiety= "Primer El"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chumakov I;
                                                                                                                                                                                                                                                 bound_moiety= "Probe P1"
/number= 1
9391..9845
/*tag= d
/note= "Amplicon 99-430"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 93-100; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 bis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 bis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13250..17590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2374..12739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             number= 1 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-IB01444.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /number= 2
                                                                                                                                                                                                              ..9506
                                                                      9391..9408
                                                                                                                                        9475..9493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'number=
                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                  *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                          /*tag=
                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200008209-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blumenfeld M,
                    misc_feature
                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-AUG-1998;
                                                                                                                                                                                                                misc_binding
                                                                      primer_bind
                                                                                                                                            primer_bind
                                                                                                                                                                                                                                                                                                                                                            primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
 ó
                                                                                                                                                                                                                                                                                                                                                                                                        AAZ32159 to AAZ32194 represent reference alleles for specifically claimed nucleic acid sequences from the present invention which comprise polymorphic sites as given in a table in the specification, selected from 92 single nucleotide polymorphisms in which the nucleotide at the polymorphic site is different from a nucleotide at the same site in a reference allele. The nucleic acids, and primers and probes, are used to identify polymorphisms, which may predispose an individual to disease, especially a vascular disease. They can also be used in phenotype correlations, forensics, paternity testing, medicine or genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TBC-1; human; biallelic marker; chromosome 4; cell cycle regulator; SNP; Single nucleotide polymorphism; tissue differentiation; prostate cancer; linkage analysis; genetic map; detection; diagnosis; genotyping; transgenic animal; screening; ds.
                                                                                                                                                                                                                                                                                                                     Determination of polymorphisms in genes, especially those identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8526 TAATITITGTATTTTAGTAGAGGIGGGTTTCACCATGTTGGCCAGGCTGGT 8474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 13865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TBC-1 partial genomic DNA comprising 5' end sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13865 BP; 3711 A; 2955 C; 3240 G; 3959 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9015 taatttttgtatttttagtagagatggggtttcaccatgttggccaggctgt
                                                                                                                                                                                                                                  Rozen SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.2%; Score 53; DB 20; 1100.0%; Pred. No. 1.7e-08; Live 0; Mismatches 0;
                                                                                                                                                                                                                              Cargill M, Ireland JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "5' Regulatory region"
                                                                                                                                                                                           (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1..2000
                                                                                                                                                                                                                                                                                                                                         predisposition to vascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to some of the reference alleles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZS0904/c
ID AAZS0904 standard; DNA; 17590 BP.
                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 9; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number= 1
2078..12739
                                                                                                                     99WO-US06473.
                                                                                                                                                          98US-0054272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...2077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53; Conservative
                                                                                                                                                                                                                              Lander ES, Daley GQ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 53; Conserva
                                                                                                                                                                                                                                                                WPI; 1999-620066/53.
                                                                                                                                                                                                                                                                                  P-PSDB; AAY49556
                  Homo sapiens
                                                 W09950454-A2
                                                                                                                       26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                    07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ50904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
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SXS

AAF97862;

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Cancer therapy; breast and ovarian cancer predisposing gene; immunogen; antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
                                                                                                                                                                                                                      Mutated BRCA1 genomic sequence from sample set MSKCC family 19921.
                  9199 TAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGT 9147
   9015 taatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt 9067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= j
fnote= "indefinite interval within intron 3"
i678..2788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **tag= f
note= "indefinite interval within intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ^*tag= n
note= "indefinite interval within intron 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       **tag= c
note= "known polymorphic site"
513...1611
*tag= d
note= "exon 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= g
fnote= "known polymorphic site"
2207..2260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= 1
/note= "known polymorphic site"
2789..3328
                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                   AAT17455 standard; cDNA; 24025 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/note= "intron 1"
1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag= e
note= "intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= i
/note= "intron 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= m
/note= "intron 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .ntron 5"
                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "exon 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= k
/note= "exon 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= h
/note= "exon 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= o
/note= "exon 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= p
/note= "int
3598..3610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612..2206
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..2677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        925..1937
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                                                                                                                                                      AAT17455;
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                                                                                    86
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                                                                                                                                                                                                                                                                                                                                                                   Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a homozygosity deletion domain co-existing in the 36-position of the first chromosome short arm (1p36) in human neuroblastoma. Also described are base sequences from the 1p36 position of human neuroblastoma cell lines (NB-1 and MASS-NB-SCH-1), which are tumour suppressor genes in human neuroblastoma. The genes are tumour suppressor genes in human neuroblastoma. The genes are tumour suppressor genes, base sequence data of which are applicable as tumour action, and gene diagnosis of tumours as well as in developing anti-cancer drugs. ARF97787 to ARF97829 represent PCR primers used in the exemplification of the present invention, and AAF97830 to AAF97824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human 1p36 homozygosity deletion domain from the 36-position of first chromosome short arm in human neuroblastoma cell lines, applicable e.g. in gene diagnosis of tumors as well as in developing anti-cancer drugs
                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome 1; 1p36; neuroblastoma cell line; NB-1; anticancer; tumour suppressor; human 1p36 homozygosity deletion domain; tumour; diagnosis; ds.
                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.2%; Score 53; DB 22; Length 22081;
100.0%; Pred. No. 1.5e-08;
ive 0; Mismatches 0; Indels 0.
                                                                                  Length 17590;
                                Sequence 17590 BP; 4760 A; 3776 C; 4104 G; 4919 T; 31 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22081 BP; 5910 A; 5508 C; 5430 G; 5233 T; 0 other;
                                                                                                                 Indels
                                                                               0.2%; Score 53; DB 21; I
100.0%; Pred. No. 1.6e-08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Page 149-158; 226pp; Japanese.
                                                                                                                                                                                                                                                                      BP.
of compounds for use in therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HISM ) HISAMITSU PHARM CO LTD.
                                                                                                                                                                                                                                                   AAF97862/C
ID AAF97862 standard; DNA; 22081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-1999; 99JP-0245962.
09-MAY-2000; 2000JP-0136266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-AUG-2000; 2000WO-JP05930.
                                                                                                                                                                                                                                                                                                                                    31-MAY-2001 (first entry)
                                                                                                                53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIB-) CHIBA PREFECTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-226686/23.
                                                                             Query Match
Best Local Similarity
Matches 53; Conserv
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Best Local Similarity
Matches 53; Conserv
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/*tag= q /note= "indefinite interval within intron 5"

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Gaps

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Conservative

invention.

| /*tag= ap /note= "known polymorphic site" 13004 /**** | | | // cay- as //note= "known polymorphic site" 1328 at /*tag= at | - | | | /note= "known polymorphic site" 14041 /*tag= ax | | /note= "known polymorphic site" 14475 - 7 | / ocs "wown polymorphic site" 14874 /*tag= ha | - | /*tag= bb /note= "known polymorphic site" 1496 | /tag= bc /note= "known polymorphic site" 1502415424 | /*tag= bd /note= "intron 11" | /*teg= be /note= "known polymorphic site" 1542515511 | /*tag= bf //note= "exon 12" 1512 15952 | /*tag= bg //note= intron 12" | /*tag= bh /nttag= bh | . 16126 | /note= "exon 13" 16077 /*tag= bj | th 0.2%; Score 53; DB 17; Length 24025; Similarity 100.0%; Pred. No. 1.5e-08; 53; Conservative 0; Mismatches 0; Indels 0; | taatttttgtatttttagtagaatggggtttcaccatgttggccaggctggt 9067 | |
|--|---|---------------------------------------|--|-----------------|------------------------------------|-----------------------------|---|-----------------------------|--|---|-----------------------|--|---|---|--|--|---------------------------------|-------------------------|---------|--|---|---|--|
| FT FT misc_feature | FT FT misc_feature FT | FT FT misc_feature FT | FT FT misc_feature FT | FT misc_feature | FT FT misc_feature FT | FT FT misc_feature FT | FT FT misc_feature FT | FT FT misc_feature FT | FT FT misc_feature FT | FT FT misc_feature FT | FT FT misc_feature | FT FT misc feature | intron | | exon | | 4 | | FT exon | FT FT misc_feature FT | Query Match Best Local Similar Matches 53; Con | Oy 9015 taatttttgt | SULT 87 |
| e 3653 /*tag= r /note= "known polymorphic site" 3814.3902 | /*tag= 8 //octe= "exon 6" 3903.4224 | /*tag= t /note= "intron 6" 4223 | | | /*tag= w //note= "exon 7" 43656571 | | o | | | /*tag= ab /note= "exon 8" 66789163 | | | 9106 /*tag= ae /note= "known polymorphic | 91649209 /*tag= af /note= "exn 9" | 9207 /*tag= ag /note= "known | 921010530 /*tag= ah /note= "intron 9" | 9376 /*tag= /note= | | | /*tag= /note= " 113841 | • | /note= "exon 11" e 11908 /*tag= an /*note= "known polymorphic site" | 11994 /*tag= ao /note= *known polymorphic 12952 |
| misc_feature exon | intron | mutation | misc feature | exon | intron | misc_feature | misc_feature | misc_feature | exon | intron | , | misc_reature | misc_feature | exou | misc_feature | intron | misc_feature | exon | intron | misc_feature | exon | misc_feature | misc_feature misc_feature |
| FT FT FT | FT FT | F F F F F F F F F F F F F F F F F F F | FT FT | FF | FFF | FT | FT FT | FT FT | FT FT | FFF | FF | FT | FT | FT FT | FT FT | FT FT | er Pr | FT | FT | | 4 4 4 4 4 | 1111 | FT FT FT |

ö 53; DB 17; Length 24025; No. 1.5e-08; matches 0; Indels 0; Gaps

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/*tag= ad
/note= "site of 1 nucleotide deletion at known
polymorphic site"
9163..9208
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note= "indefinite interval within intron 10"
1597..15022
                                                                                                                                                  /*tag= x

/note= "known polymorphic site"

1602..4614

/*tag= y

/*tag= "indefinite interval within intron 7"

5538
                                      **tag= u
'note= "indefinite interval within intron 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= ap
/note= "known polymorphic site"
13008
/*tag= aq
/note= "known polymorphic site"
13047
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9209..10529
/*tag= ag
/note= "intron 9"
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note= "known polymorphic site"
0530..10606
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note= "known polymorphic site"
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note= "known polymorphic site"
106
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2951
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'note= "known polymorphic site"
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"known polymorphic site"
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/note= "exon 10"
10607..11596
/*tag= aj
/note= "intron 10"
11383..11395
/*tag= t
/note= "intron 6"
4076..4088
                                                                        /*tag= v
/note= "exon 7"
4365..6571
/*tag= w
/note= "intron 7"
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note= "intron 8"
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/note= "exon 11"
11907
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/note= "exon 8"
6678..9163
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/note= "exon 9"
9206
                                                              225..4364
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note=
1993
                         misc_feature
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                                                                                                Cancer therapy; breast and ovarian cancer predisposing gene; immunogen; antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
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/note= "known polymorphic site"
207..260
/*tag- h
/note= "exon 3"
2561..2677
/*tag- i
/note= "intron 3"
2569..2581
/*tag- k
/note= "indefinite interval within intron 3"
2678..2788
/*tag- k
/*tag- k
/*tag- k
                                                                                                                                                                                                                                                                         /*tag= c
/note= "known polymorphic site"
1513..1611
/*tag= d
/note= "exon 2"
1612..2206
/*tag= e
/note= "intron 2"
1925..1937
/*tag= f
/note= "indefinite interval within intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= r
/note= "known polymorphic site"
3814..3902
/*tag= s
/note= "exon 6"
3903..4224
                                                                        Mutated BRCAl genomic sequence from PM15.
                                                                                                                                                                         Location/Qualiflers
256..355
AAT17515 standard; cDNA; 24025 BP
                                                                                                                                                                                                                                       *tag= b
note= "intron 1"
295
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/note= "exon 1"
356..1512
                                               04-OCT-1996 (first entry)
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BRCA1; breast cancer; ovary cancer; predisposing gene; chromosome 17q;
               susceptibility gene; diagnosis; prognosis; gene therapy; gene mapping; marker; testis; thymus; exon; intron; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note "n at 11383-11396 represent an indefinite interval within the intron" 11598..15023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= y
/note= "n at 15647-15659 represent an indefinite
                                                                                                                             /*tag= e
/note= "n at 1925-1937 represent an indefinite
interval within the intron"
                                                                                                                                                                                                                      /*tag= i
/note= "n at 3063-3075 represent an indefinite
3329..3406
/*tag= j
3407..3813
/*tag= "n at 3598-3610 represent an indefinite
                                                                                                                                                                                                                                                                                                              /*tag= m
/note= "n at 4076-4088 represent an indefinite
interval within the intron"
                                                                                                                                                                                                                                                                                                                                                 /*tag= o
/note= "n at 4602-4614 represent an indefinite
interval within the intron"
6572..6677
                                                                                                                                                          /*tag= f
2261..2677
/*tag= g
/note= "n at 2569-2581 represent an indefinite
interval within the intron"
                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= v
15024..15424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= x
15512..15952
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10531..10607
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9208..10530
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6678..9163
/*tag= q
9164..9207
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1513..1611
/*tag= d
1612..2206
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2789..3328
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4365..6571
/*tag= o
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3903..4224
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156..1512
/*tag= c
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10608..]
/*tag=
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15425...
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                                      Homo sapiens
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note- "indefinite interval within intron 12"
5952..16125
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44045
/*tag= ax
//tag= "known polymorphic site"
14474
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/note= "known polymorphic site"
16126..16564
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"known polymorphic site"
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"known polymorphic site"
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'note= "intron 12"
5646..15658
                                                                                                                                                                                                                                                           "intron 11"
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                                                  "known
                             "known
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/note= "known
15023..15423
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/note= '
13950
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/note= '
14040
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14890
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13237
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14965
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16076
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Matches
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ID AAT3

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100.0%; Pred. No. 1.5e-08;
tive 0; Mismatches 0;
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13539 bm
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|376
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1994
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3238
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'note= "polymorphic site"
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"polymorphic
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Best Local Similarity 100.0
Matches 53; Conservative
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/note= '
11908
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207
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     /*tag= aa
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interval within the intron"
                                                                                                                                                                                                              /*tag= af
18788..19298
/*tag= ag
/note= n at 18952-18964 represent an indefinite
interval within the intron"
                                                                                                                 force "n at 17290-17302 represent an indefinite interval within the intron" .7536..17726
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interval within the intron"
23699...24026
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interval within the intron" 15953..16126
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/note= "polymorphic site"
3653
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/*tag= ac
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23349..23698
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17727..1
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22907..2
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16127..
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| misc_feature | /*tag= /note= " exon 657266 | FI //cay= ad | misc_feature 6823 /*tag= ac /*tag= ac /*note= "known p | exon | misc_feature | /reg= /note= intron 9210 | misc_feature | /note= " exon 105311 /*tag= | intron | /notes /notes misc_feature 113841 | /note=" exon 115981 /*tag= | /note= " misc_feature 11908 /*tag= | /note= "/note=" /note=" /note= | misc_feature 12952 | / cay /note= misc_feature 13004 | FT //tag= ap //note="known polymorphic site" FT misc_feature 13009 | misc feature | sc feature | misc feature | | FT /*tag= au /*tag= au /*tag= n/ /*tag= nu /*tag= FT misc_feature 13951 | |
|--|---|--------------|--|------|--------------|--|--|--|---|--|--|---|--|--|---------------------------------------|--|--|--|---|-----|---|--|
| Location/Qualifiers 256355 /*tag= "exon 1" | intron 3561512 /*tag= b //note= "intron 1" misc feature 1905 | | /note= "exon 2" 16122206 /tag= e //note= "intron 2" | c | | /*tag=_rcch /note= "exon 3" 22612677 | /*tag= i /note= "intron 3" misc_feature 25692581 | /*tag= ; //octe= indefinite interval within intron 3" 2678.,2788 | /*tag= k //note= "exon 4" misc_feature 2725 | /*tag= 1 /otce= "known polymorphic site" 2789 3328 | /*tag= m //*tag= m //note= "intron 4" misc_feature 3063.3075 | /*tag= n /note= "indefinite interval within intron 4" 3329.3406 | /*tag= o //note= "exon 5" 3407.3813 | /*tag= p /*t |) | misc_reature 3653 //rtag= r /note= "known polymorphic site" | 38143902 /*tag= s /note= exon 6" | 39034224 /#tag- t //note= "intron 6" | misc_feature 40764088 /tag= u /ndefinite interval within intron 6" | 7.8 | /3656571 /*tag= w /note= "intro | misc_feature 43914392 //rtag= // / / / / / / / / / / / / / / / / / |

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/ttgg x /note= "known polymorphic site"
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//ttag y /note= "indefinite interval within intron 7"
6538
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note- "indefinite interval within intron 4"
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note= "indefinite interval within intron 5"
653
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             *tag= c
note= "known polymorphic site"
513..1611
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6572..6677
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note= "known polymorphic site"
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814.3902
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1925..1937
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/note= "C to A mutation at known polymorphic site"
15425..15511
/*tag= "exon 12"
/*5512..15552
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note= "indefinite interval within intron 12"
5953..16126
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100.0%; Pred. No. 1.5e-08;
tive 0; Mismatches 0; Indels 0
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/note= "known polymorphic site"
16127..16565
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"known polymorphic site"
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5024..15424
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note= "known polymorphic site"
                                            "known polymorphic site"
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5647..15659
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note= "exon 13"
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Matches 53; Conservative
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4966
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Cancer therapy; breast and ovarian cancer predisposing gene; immunogen; antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
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note= "Indefinite interval within intron 12"
5953..16126
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/note= "known polymorphic site"
|1513..1611
/*tag= d
/note= "exon 2"
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16127..16665
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5425..15511
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  "known polymorphic site"
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256..355
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16077
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1295
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/note= "exon 1"
356..1512
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/note= "exon 11"
/*tag- am
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//*tag= "known polymorphic site" .
//*tag= ai //*tag= 
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/note= "known polymorphic site"
13448
/*tag= at
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1612..2206
/*tag= e
/note= "intron 2"
1925..1937
/*tag= f
/note= indefinite interval within intron 2"
2141
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[5953..16126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 24026;
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11 Similarity 100.0%; Pred. No. 1.5e-08;
53; Conservative 0; Mismatches 0;
                           bb
"known polymorphic site"
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16127..16565
/*tag= bj
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note= "known polymorphic site"
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256..355
                                                                                                                           'note= "intron 11"
.5284
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.295
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16077
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'note= "exon 1"
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AAT17516;

92

RESULT 9

intron

exon

Key

intron

exon

Query Match

Matches

intron

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15647..15659
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1295
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16077
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356..1512
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//*tag= ap
//*tag= ap
//*ote= "known polymorphic site"
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//*tag= aq
//note= "known polymorphic site"
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13448
/*tag= at
/note= "known polymorphic site"
13539
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/*tag- aw
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/*tag- ax
 /*tag= af
/note= "known polymorphic site"
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2952
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3238
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3951
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4475
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4966
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5024..15424
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4874
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15284
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9376
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'note= "
1994
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note="G to A mutation at known polymorphic site"
:513..1611
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[5953..16126
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1627..16565
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15425..15511
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/note= "known polymorphic site"
2207..2260
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256..355
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| FT /*tag= ah /*tag= ah /*tag= ah //note= "known polymorphic site" FT exon 1053110607 FT /*tag= ai //note= "exon 10" FT intron 1060811597 FT /*tag= aj //note= "intron 10" FT misc feature 1134411396 | <pre>"ttgg ax</pre> | /note= "known polymorphic site 11994 an //stag= an /note= "known polymorphic site 12952 //stag= ao //note= "known polymorphic site misc_feature 13004 //stag= ap | misc_feature 13009 misc_feature 13009 /*tag= aq /*tag= ad /*tag= ar /*tag= ar /*tag= ar /*tag= ar /*tag= as /*tag= as | misc_feature misc_feature misc_feature | misc_feature 14041 *tag= aw /note= "known polymorphic 14046 /*tag= ax /note= "known polymorphic 14405 /note= "known polymorphic /note= "known polymorphic /note= "known polymorphic /note= "known polymorphic | FT misc_feature 14891 ba |
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106
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076..4088
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16077
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16127..16565
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                                                                                                                                                                         Query Match 0.2%; Score 53; DB 17; Length 24026; Best Local Similarity 100.0%; Pred. No. 1.5e-08; Matches 53; Conservative 0; Mismatches 0; Indels 0;
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//tag= j
//note= "indefinite interval within intron 3"
2678..278
//tag= k
//note= "exon 4"
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note= "known polymorphic site"
513..1611
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256..355
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1612..2206
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15647..15659
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356..1512
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1295
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2569..2581
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note= "exon 3"
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Cancer therapy; breast and ovarian cancer predisposing gene; immunogen; antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
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                                                               Length 24026;
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note= "intron 2"
1925..1937
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678..2788
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/octe= hitron 4"
3063..3075
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16077
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256..355
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| misc_feature misc_feature misc_feature misc_feature | misc_feature exon misc_feature exon intron misc_feature exon exon exon exon exon exon | misc_feature intron Query Match |
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1384..11396
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1164..9209
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106
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4076..4088
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note= "exon 6"
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/note- "exon 3"
2261..267
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/*tag- indefinite interval within intron 3"
2578..2788
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Best Local Similarity 100.0%; Pred. No. 1.5e-08; Matches 53; Conservative 0; Mismatches 0;
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256..355
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Cancer therapy; breast and ovarian cancer predisposing gene; immunogen; antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
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/note= "intron 4"
3063.3075
/*tag= n
329..3406
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note= "indefinite interval within intron 2"
                                                                                                                                                                                                                                                                             /*tbg= c
/note= "known polymorphic site"
1513..1611
/*tag= d
/note= "exon 2"
[111..2206
/*tag= e
/note= "intron 2"
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note= "known polymorphic site"
789..3328
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/note= "known polymorphic site"
3814..3902
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note= "known polymorphic site"
(207..2260
                                                                                                 Mutated BRCAl genomic sequence from PMA08.2.
                                                                                                                                                                                        Location/Qualifiers
256..355
                                                                                                                                                                                                                                           /*tag= b
/note= "intron 1"
!295
                                AAT17522 standard; cDNA; 24026 BP
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/note= "exon 5"
3407..3813
                                                                                                                                                                                                               *tag= a
note= "exon 1"
                                                                            (first entry)
                                                                                                                                                                                                                                  356..1512
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note= "indefinite interval within intron 12"
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Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 53; Conservative 0; Mismatches 0;
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16127..16565
/*tag- bj
ao
"known polymorphic site"
                                                              *tag= aq
note= "known polymorphic site"
3048
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note= "known polymorphic site"
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"known polymorphic site"
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note= "known polymorphic site"
4046
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/note= "intron 12"
15647..15659
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note= "intron 11"
5284
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/note= "known poly
15425..15511
/*tag= be
/note= "exon 12"
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16077
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/note= "known
15024..15424
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'note=
13951
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note=
3539
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note= "intron 12"

5447..15699

*tag- "indefinite interval within intron 12"

5553..16126
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/note= "known polymorphic site"
113951
/*tag= av
/note= "known polymorphic site"
14041
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/note= "known polymorphic site"
1504..15424
/*tag= bc
/note= "intron 11"
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/note= "known polymorphic site"
|15425..15511
/*tag= be
/note= "exon 12"
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/note= "known polymorphic site"
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note= "known polymorphic site"
4966
                    "known polymorphic site"
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note= "exon 13"
6077
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note=
4475
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note=
3448
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4874
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3238
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AC AAT1752
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hote= "A to T mutation at known polymorphic site"
106
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/*tag= s
/note= "exon 6"
3903. 4224
/*tag= "intron 6"
4076. 4088
/*tag= "indefinite interval within intron 6"
/425. 4364
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/note= "known polymorphic site"
/210.10530
/*tag= ag
/note= "intron 9"
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//note= "known polymorphic site"
13009
/*tag= aq
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note- "known polymorphic site"
1164..9209
*tag- ae
note- "exon 9"
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/note= "known polymorphic site"
13004
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note= "known polymorphic site"
1994
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note= "known polymorphic site"
2952
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note= "known polymorphic site'
572..6677
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/note= "exon 8"
fors...9163
f*tag= ab
/note= "intron 8"
6823
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Gaps

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*tag= ah note= "T to C mutation at known polymorphic site" 0531\dots10607
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note= "indefinite interval within intron 10"
1598..15023
 'note= "indefinite interval within intron 6"
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note= "indefinite interval within intron 7"
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note= "known polymorphic site"
106
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note= "known polymorphic site"
164..9209
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note= "known polymorphic site"
602..4614
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'note= "known polymorphic site"
5572..6677
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210..10530
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376
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note= "known polymorphic site"
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note= "known polymorphic site"
3048
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/note= "intron 10"
11384..11396
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/note= "exon 7"
4365..6571
/*tag= w
/note= "intron 7"
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/note= "exon 10"
10608..11597
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note= "intron 8"
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note= "intron 9"
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/note= "exon 9"
3207
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5678..9163
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note= "exon 11"
1908
              225..4364
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2789.328
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1612..2206
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3814..3902
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                                                                                                                                         Socation/Qualifiers
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356..1512
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1295
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4076..4088
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04-OCT-1996 (first entry)
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1076.4088

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256..355
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'note= "intron 1"
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note= "exon 7"
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15647..15659
/*tag= bg
15953..16126
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note= "known polymorphic site"
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14874
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"known polymorphic site"
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3951
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16077
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Cancer therapy; breast and ovarian cancer predisposing gene; immunogen; antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
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Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 53; Conservative 0; Mismatches 0;
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15284
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| GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen OM nucleic - nucleic search, using sw model Run on: November 1, 2001, 21:14:50; Search (without | S-09-434-382-28 6664 tatcaggtgactgaattcta LIGO_NUC apop 60.0 , Gapext 60.0 24599 segs, 94655562 residues | Word size: Word size: Total number of hits satisfying chosen parameters: Minimum DB seq length: 00 Maximum DB seq length: 100000000 Post-processing: Listing first 100 summaries Database: Issued_Patents_NA:* I: /cgn2_6/ptcdata/2/ina/5B_COMB.seq:* 3: /cgn2_6/ptcdata/2/ina/6B_COMB.seq:* 4: /cgn2_6/ptcdata/2/ina/6B_COMB.seq:* 5: /cgn2_6/ptcdata/2/ina/6B_COMB.seq:* 6: /cgn2_6/ptcdata/2/ina/fbB_COMB.seq:* 6: /cgn2_6/ptcdata/2/ina/fbB_COMB.seq:* 6: /cgn2_6/ptcdata/2/ina/pcTuS_COMB.seq:* | Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score of the and is derived by analysis of the total score of the and is derived by analysis of the total score of the and is derived by analysis of the total score of the and is derived by analysis of the total score of the and is derived by analysis of the total score of the and is derived by analysis of the total score of the analysis of the total score of tota |

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APPLICANT: DUFF, GORDON W.
APPLICANT: DUFF, GORDON W.
APPLICANT: CAMP, NICOLA J.
APPLICANT: CAMP, NICOLA J.
APPLICANT: DIGIOVINE, FRANCESCO S.
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISBASES ASSOCIATED
TITLE OF INVENTION: WITH AN IL-1 INFLAMMATORY HAPLOTYPE
FILE REFERENCE: MSA-010, 02
CURRENT APPLICATION NUMBER: DS/09/345,217
CURRENT FILING DATE: 1999-06-30
EARLIER PLING DATE: 1999-06-30
EARLIER PLING DATE: 1999-06-30
EARLIER PLING DATE: 1999-06-30
SALIER PLING DATE: 1997-05-29
SECULOR OF SEQ ID NOS: 32
SOFTWARE: PETCHIN VOET: 2.0
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                                                                                                                                               GENERAL INFORMATION:
APPLICANT: KELLEMS, RODNEY E.
APPLICANT: BATAA SURAIT K.
APPLICANT: BATAA SURAIT K.
APPLICANT: BATAA SURAIT K.
TITLE OF INVENTION: METHODS FOR THE USE THEREOF
FILE NEFFERENCE: UTSH:243
CURRENT FILING DATE: 1999-04-28
EARLIER FILING DATE: 1998-04-28
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MUMBER OF SEQ ID NOS: 4
SOFTWARE: PATCHING VET: 2.0
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, OTHER INFORMATION: other or unknown
US-09-345-217-2
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Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 61; Conservative 0; Mismatches 0; Indels
ALIGNMENTS
                                                                                                            Sequence 3, Application US/09301665 Patent No. 6207876
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Patent No. 6268142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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US-09-301-665-3
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US-09-345-217-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                                                                                           Sequence 16, Application US/09128155

Patent No. 6117654

GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROFEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER PILING DATE: 1998-07-02
EARLIER PILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 152331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oy 11740 tttttttgagacagagtctcactctgtcgcccaggctggagtgcagtggcacgatctcgg 11799
                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PAN: Yang
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: 1904-05-001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/094,646
EARLIER FILING DATE: 1998-07-08
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastERO for Windows Version 3.0
SEQ ID NO 17
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     Length 9721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.2%; Score 60; DB 3; Le Best Local Similarity 100.0%; Pred. No. 6.9e-14; Matches 60; Conservative 0; Mismatches 0;
Query Match 0.2%; Score 60; DB 4; L
Best Local Similarity 100.0%; Pred. No. 9.4e-14;
Matches 60; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-128-155-17; Sequence 17, Application US/09128155; Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature

| LOCATION: (1)...(152331)

| OTHER INFORMATION: n = A,T,C or G

US-09-128-155-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature

| LOCATION: (1)...(176373)

| CTHER INFORMATION: n = A,T,C or G

US-09-128-155-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 176373
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US-09-128-155-16
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US-08-658-136-2; Sequence 2, Application US/08658136; Patent No. 6071717
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                                                                                                                    0; Gaps
                                      0.2%; Score 60; DB 3; Length 176373;
100.0%; Pred. No. 6.8e-14;
ive 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DACKOWSKI, WILLIAM R.
APPLICANT: DACKOWSKI, WILLIAM R.
APPLICANT: GERMINO, GREGORY
APPLICANT: OIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,443B FILING DATE: 12-OCT-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0372/0A462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   Sequence 1, Application US/08323443B
Patent No. 5654170
                                                                                                                                                                                                                                                                                                                          APPLICANT: KLINGER, KATHERINE W.
PSPLICANT: LANDES, GREGORY M.
APPLICANT: BURN, TIMOTHY C.
APPLICANT: CONNORS, TIMOTHY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFRENCE/DOCKET NUMBER: 0372,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHERICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 31571 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                           Local Similarity 100.
hes 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: PKD1 GENOMIC
US-08-323-443B-1
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic
STRANDEDNESS:
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                                                                                                                                                                                                                                              US-08-323-443B-1
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STATE: N
COUNTRY:
                                          Query Match
                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: BURN, TIMOTHY C
APPLICANT: BURN, TIMOTHY D
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: OIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
GENERAL INFORMATION:
APPLICANT: LANDES, GREGORY M
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: BURN, TIMOTHY C
APPLICANT: BURN, TIMOTHY D
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSED. GENEVALUE CONTOUR ADDRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                 ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENZYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-658-136-1; Sequence 1, Application US/08658136; Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: DNA (genomic) US-08-658-136-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: ONE MOUNTAIN ROAD CITY: FRAMINGHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 53526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                    CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                            01701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION:
TELEPHAN: 212-758-2400
TELEFAX: 212-758-2982
                                                                                                     TELEX: 236262
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2688 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                        CDS
358 to 486
560 to 799
1042 to 1182
2105 to 2269
2370 to 2462
                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                    ORGANISM: human
IMMEDIATE SOURCE:
CLONE: F55
                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
LOCATION:
LOCATION:
                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                    FEATURE
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CITY: New York

CITY: New York

COUNTRY: U.S.A.

ZIP: 10172-0194

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/909,965C

FILING DATE: August 12, 1997

FILING DATE: August 12, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nakagawa Satoshi
APPLICANT: Nakagawa Satoshi
APPLICANT: Sakaki yoshiyuki
APPLICANT: Sakaki yoshiyuki
APPLICANT: Bashida Hideji
TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE
TITLE OF INVENTION: AND NOVEL ANTIBODY
NUMBER OF SEQUENCES: 17
CORRESSONDENCE ADDRESS:
ADDRESSEE: FITZPATRICK, CELLA, HARPER AND SCINTO
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION NUMBER: US/08/658,136
FILING ATTON NUMBER: BIZABETH
REGISTRATION NUMBER: 31.845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUTICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEPAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 53577 Dasse pairs
TYPE: NOULDED SEG SIDGLE
STRANDEDDESS: SIDGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

0.2%; Score 59; DB 3; Le
Best Local Similarity 100:0%; Pred. No. 1.9e-13;
Matches 59; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 322745/95
APPLICATION NUMBER: PCT/JP96/03630
FILING DATE: 12-No. 5936078-1995
FILING DATE: 12-Dec-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-909-965C-1/c
; Sequence 1, Application US/08909965C
; Patent No. 5936078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-658-136-1
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GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STAVEN A.

APPLICANT: STAVEN A.

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHONS
TITLE OF INVENTION: METHONS
INTERED: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPUTER: DSACII
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/417,174
FILING DATE: 05-APR-1995
FILING DATE: 22-APR-1994
CLASSITICATION: 435
                                                                                     Query Match 0.2%; Score 58; DB 2; Length 2688; Best Local Similarity 100.0%; Pred. No. 6.2e-13; Matches 58; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REPERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
; IDENTIFICATION METHOD: by experiment US-08-909-965C-1
                                                                                                                                                                                                                                                                                                RESULT 9
US-08-417-174-1
Sequence 1, Application US/08417174
; Patent No. 5844075
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Qy 12671 gttggtcaggctggtctcaaactcctgacctcaggtgatctgcccgcctcagcctcc 12727
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                                                                                    Sequence 1, Application US/09007961

Sequence 1, Application US/09007961

Septent No. 594523

GENERAL INFORMATION:
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCE: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08370975B
Patent No. 5622851
GENERAL INFORMATION:
APPLICANT: Maley, Frank
APPLICANT: Maley, Gladys F.
APPLICANT: Weiner, Karen X.B.
ATITLE OF INVENTION:
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 1.6e-12; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.2%; Score 57; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/007,961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08/231,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/POCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                             345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.C
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 751-68-
TELEX: 421792
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                         ADDALL
STREET: 345 ...
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNKNOMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEOTIDE STRANDEDNESS: DOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Clinton
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: UN
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                10154
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US-08-370-975B-6
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COUNTRY:
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CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                           0.2%; Score 57; DB 2; Length 1559;
100.0%; Pred. No. 1.6e-12;
Live 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.6e-12;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565A
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08231565A Patent No. 5874560 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFRENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1559
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                        TYPE: NUCLEOTIDE
STRANDEDNESS: DOUBLE
TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Thes 57; Conserva'
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MOLECULE TYPE:
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MOLECULE TYPE:
US-08-417-174-1
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STATE: NI
COUNTRY:
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Length 1559;

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APPLICANT: Wiseman, Roger A.
APPLICANT: Futreal, P. Andrew TITLE OF INVENTION: 179-Linked Breast and Ovarian Cancer TITLE OF INVENTION: Susceptibility Gene NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS: About Surfact Andrew For Street Surfact Surfa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,784
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CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24 MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-MOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,221
APPLICATION NUMBER: US 08/209,221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Swenson, Jeff
Kamb, Alexander
Harshman, Keith D.
Shattuck-Eidens, Donna M.
Tavtigian, Sean V.
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                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 4435
US-08-370-975B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skolnick, Mark H.
Goldgar, David E.
Miki, Yoshio
   INFORMATION FOR SEQ ID NO: 1:
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 26764 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 12-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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STATE:
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Patent No. 5622851
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Maley, Frank
APPLICANT: Meiner, Karen X.B.
TITLE OF INVENTION: Human Deoxycytidylate Deaminase Gene
                                                                                                                                      MEDIUM TYPE: RICHPY LLS.
COMPUTER: BLM PC compatible
COMPUTER: DEAD PC COMPAGE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,975B
FILING DATE: 10-JAN-1995
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REGISTRATION NUMBER: 34,103
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1660
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHRARATISTICS:
SEQUENCE CHRARACTERISTICS:
SEQUENCE CHRARACTERISTICS:
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SOFTWARE PATENTIN Belease #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/370,975B

FILING DATE: U0-JAN 1995

CLASSIFICATION: 435

ATONREY/AGENT INPORMATION:

NAME: Tinian, Susan 34,103

REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 20894/80

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 10F0RMATION:

TELECOMMUNICATION 10F0RMATION:

TELECOMMUNICATION 10F0RMATION:

TELECOMMUNICATION 10F0RMATION:
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ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                        ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 20303 base pairs TYPE: nucleic acid
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CHROMOSOME/SEGMENT: 4q35
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New York
                                      USA
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STRANDEDNESS:
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US-08-370-975B-1
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ORGANISM:
0S-08-483-553-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 179-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: SASCEPTIBILITY Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2: Venable, Baetjer, Howard & Civiletti, LLP
1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHILR Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/483,553
REFERENCE/DOCKET NUMBER: 24884-109347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Mikl, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Harshman, Keith D.
APPLICANT: Tavtigian, Sean V.
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FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 29-MOV-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/08483553
Patent No. 5709999
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
             TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                   HYPOTHETICAL: NO
MATI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO sapiens
US-08-480-784-20
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
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US-08-483-553-20
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Gaps
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APPLICANT: Shard, Jacques
APPLICANT: Shard, Jacques
APPLICANT: Bai, Mitsuru
APPLICANT: Durocher, Francine
APPLICANT: Durocher, Francine
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OFFWARE: PatentIn Release #1.0, Version #1.30 CARRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 1; LA Pred. No. 4.4e-11;
                                                             NAME: Thnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.2%; Score 53; DB Best Local Similarity 100.0%; Pred. No. 4.4 Matches 53; Conservative 0; Mismatches
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APPLICATION NUMBER: US 08/289,221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/487,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-487-002-20
; Sequence 20, Application US/08487002
; Patent No. 5710001
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                             FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                              TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                  잁
                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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9015 taatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt 9067
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APPLICANT: Mixi, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Swenson, Jeff
APPLICANT: Ramb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 1/9-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCES: 85
CORRESPONDENCES: 86
CORRESPONDENCES: Batjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 6769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.2%; Score 53; DB 1; Length 676
100.0%; Pred. No. 4.4e-11;
tive 0; Mismatches 0; Indels
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                                                                             PFILING DATE: 10-75F-1394

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/300,266

FILING DATE: 02-SEP-1994

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/289,221

FILING DATE: 12-AUG-1994

ATTORNEY/AGENT INFORMATION: AMME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957

REEFRENENCY/DOCKEY NUMBER: 24884-109347

FELECOMMUNICATION INFORMATION: TELEPHONE: 202-962-4810

INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 6769 base pairs
                                            UMBER: US 08/308,104
16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/08488011B Patent No. 5753441
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Goldgar, David E.
Miki, Yoshio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
FILING DATE: 29-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Best Local Similarity 100.
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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APPLICANT: Skolnic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
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                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM:
US-08-483-554B-20
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US-08-488-011B-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.2%; Score 53; DB 1; Length 6769; Best Local Similarity 100.0%; Pred. No. 4.4e-11; Matches 53; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-406-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2484-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
INFORMATION FOR SED ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRENDEDNESS: Gouble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Rashman, Keith D.
APPLICANT: Bhattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/483,554B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 08/348,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08483554B Patent No. 5747282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
DATE: 02-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-483-554B-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
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us-09-434-382-28.oli.rni

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APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Bai, Mitsuru
APPLICANT: Nakamura, Yusuke
APPLICANT: Nakamura, Yusuke
APPLICANT: Invention: In Vivo Mutations and Polymorphisms
TITLE OF INVENTION: In the 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.2%; Score 53; DB 4; Length 6769;
100.0%; Pred. No. 4.4e-11;
tive 0; Mismatches 0; Indels
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                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24884-109347
                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/850,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US95-10202-20; Sequence 20, Application PC/TUS9510202; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFRENCE/DOCKET NUMBER: 2488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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Best Local Similarity 100.0
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
CRGANISM: HOM
US-08-850-727-20
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                                                                                                                                                FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Harshman Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Wiseman, Roger W.
APPLICANT: Wiseman, Roger W.
APPLICANT: Fureal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: Venable, Baetjer, Howard & Civiletti, LLP : 1201 New York Avenue, N.W., Suite 1000 Washington
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: US 08/300,266
FILING DATE: US 08/300,266
FILING APPLICATION NUMBER: US 08/209,21
FILING DATE: US 08/209,221
FILING APPLICATION NUMBER: US 08/289,221
FILING APPLICATION NUMBER: US 08/209,21
FILING APPLICATION NUMBER: US 08/209,21
FILING APPLICATION NUMBER: 28,957
FILING APPLICATION INFORMATION:
NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 24884-109347-09
TELEPAX: 202-962-4810
TELEPAX: 202-962-4810
TELEPAX: 202-962-4810
TELEPAX: 202-962-4810
TELEPAX: 202-962-4810
TELEPAX: 202-962-8100
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Patent No. 6162897
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: GOLGGAF, David E.
APPLICANT: Miki, Yoshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skolnick, Mark H.
Goldgar, David E.
Miki, Yoshio
Swenson, Jeff
Kamb, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 53; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
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APPLICANT:
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100.0%; Pred. No. 4.4e-11;
ive 0; Mismatches 0; Indels
                                    ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CAURENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24884-109347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US
FILING DATE: 07-UN-1995
FILING DATE: 07-UN-1995
FILING DATE: 27-UN-1995
FILING DATE: 24-MAR-1995
FILING DATE: 24-MAR-1995
FILING DATE: 24-MAR-1995
FILING DATE: 29-NOV-1994
FILING DATE: 29-NOV-1994
FILING DATE: 19-NOV-1994
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PALLON NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATE: 02-SEP-1994
PRIOR APPLICATION DATE: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-962-4810
TELECHONE: 202-962-4810
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PCT-1022-20
PCT-10595-10220-20
PCT-10595-10220-20
PCT-10595-10220
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 6769 base pairs
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Best Local Similarity 100.0
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: double
         CORRESPONDENCE ADDRESS:
                                                                                                   Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                  USA
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                                                                  STREET: 120
CITY: Washi
STATE: DC
                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-10203-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 179-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: 80sceptibility Gene
NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 0.2%; Score 53; DB 5; Le Best Local Similarity 100.0%; Pred. No. 4.4e-11; Matches 53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24884-109347
                                                                                                                                                                                                                PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: US 08-308,104
FILING DATE: 16-5EP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-5EP-1994
PRIOR APPLICATION NUMBER: US 08/289,221
REGISTATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harshman, Keith D.
Shattuck-Eidens, Donna M.
Tavtigian, Sean V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application PC/TUS9510203
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET UNMBER: 2488
TELECOMMUNICATION INFORMATION:
TELEFONE: 202-962-4810
TELEFAX: 202-962-4810
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 6769 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o
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ORGANISM: HOM
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                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US95-10202-20
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APPLICANT:
APPLICANT:
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APPLICANT:
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Sequence 5, Application US/09318448
Patent No. 6210950
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-318-448-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tartigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: Method for Diagnosing a
TITLE OF INVENTION: Predisposition for Breast and Ovarian Cancer
TITLE OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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100.0%; Pred. No. 4.4e-11;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                 E: Venable, Baetjer, Howard & Civiletti, LLP 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24884-109347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDER:
SPELICATION UNDER:
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 19-5EP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 16-5EP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
RECISTRATION NUMBER: 28,957
RECISTRATION NUMBER: 28,957
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: 202-962-4810
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APPLICATION NUMBER: PCT/US95/10220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 6769 base pairs
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Best Local Similarity 100.
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                 Washington
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                                                                                                                                                                                                                                                                                                               20005
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RESULT

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Sequence 11, Application US/09009217
Patent No. 6132729
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Gao, Boning
TITLE OF INVENTION: COMBINED TISSUE FACTOR AND
TITLE OF INVENTION: CHEMOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION
TITLE OF INVENTION: AND TUMOR TREATMENT
NUMBER OF SEQUENCES: 27
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                                                                                 PREVENTING, AND TREATING
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.2%; Score 53; DB 4; La
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 53; Conservative 0; Mismatches 0;
GENERAL INFORMATION:
APPLICANT: Johnson, William G.
APPLICANT: Johnson, William G.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PR.;
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROGRAPHICATION DATA:
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PROR APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: P.O. Box 4433
CITY: Houston
STATE: Teven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/009,217 FILING DATE: Concurrently Herewith
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/474-7577
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Gaps

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9015 taattittgtatttttagtagagatggggtttcaccatgttggccaggctggt 9067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 72928;
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0. 3.4e-11; Indels
0; Indels
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Sequence 79, Application US/08781891
Sequence 79, Application US/08781891
Sequence 79, Application US/08781891
SEMERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenbergy, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA.
APPLICATION WOMBER: US/09/009,913
FILING DATE: 21-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.2%; Score 53; DB 100.0%; Pred. No. 3.4 tive 0; Mismatches
0; Mismatches
                                                                                                                                                                                                                                  APPLICANT: AxyS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
                                                                                                                                                                            Sequence 1, Application US/09009913
Patent No. 6087485
                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sherwood, Pamela J
RECISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 72928 base pairs
LENGTH: 72928 acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Genomic DNA US-09-009-913-1
53; Conservative
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Best Local Similarity 100.
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                          US-09-009-913-1
Matches
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APPLICANT: Thorpe, Philip E.

APPLICANT: Thorpe, Steven W.

APPLICANT: King, Steven W.

APPLICANT: Gao, Boning

TITLE OF INVENTION: COMBINED TISSUE FACTOR AND FACTOR VIIA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR

TITLE OF INVENTION: TREATMENT

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                    9015 taatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt 9067
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                                                                                                                                                                        Length 13865;
                                                                                                                                                        Score 53; DB 3; Length Lour Pred. No. 4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDEPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/009,656
FILING DATE: Concurrently Herewith
                                                                                                                                                                        Query Match 0.2%; Score 53; DB Best Local Similarity 100.0%; Pred. No. 4e-Matches 53; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TLING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036, 205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035, 920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UTSD:537
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09009656
Patent No. 6132730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.2%; 8
INFORMATION FOR SEQ ID NO: 11:
                              LENGTH: 13865 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 13865 base pairs
                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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Best Local, Similarity
                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                   RESULT 25
US-09-009-656-11/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                              TOPOLOGY:
                                                                                                                 US-09-009-217-11
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Patent No. 5840491
CENERAL INFORMATION:
CAPPLICANT:
CAPPLICANT:
CAPPLICANT:
CAPPLICANT:
CAPPLICANT:
CAPPLICANT:
CAPPLICANTION:
CAPPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OFTRAING SISIEM: EVENOS/MS.DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,927B
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19 H6-251600
FILING DATE: 21-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Grannan, Particia
NEGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 0.2%; Score 52; DB 2; L Best Local Similarity 100.0%; Pred. No. 1.3e-10; Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.2%; Score 52;
                                REFERENCE/DOCKET NUMBER: ATH95-01A TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240 TELEPHOXE: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   REGISTRATION NUMBER: 32,227
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                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-531-927B-9
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SEQUENCE CHARACTERISTICS:
TRNGTH: 1776 basis
                                                                                                                                  TELEFAX: 617-861-9540
INFORMATION FOR SEO ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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36..1115
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ZIP: 02173-4799
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US-08-531-927B-1/c
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US-08-531-927B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
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Patent No. 5840491
GENERAL INFORMATION:
APPLICANT: KARIZUKA, AKITA
TITLE OF INVENTION: DNA Sequence Encoding the Machado-Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.2%; Score 53; DB 3; Length 87350;
100.0%; Pred. No. 3.3e-11;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5840491
TITLE OF INVENTION: Disease Gene and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARES PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,927B
FILING DATE: 21-SEP-1995
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP H6-251600
FILING DATE: 21-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                 ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-631
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 87350 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.29
Best Local Similarity 100.0
Matches 53; Conservative
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STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                   STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                         Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.2%; Score 52; DB 1; Length 17327;
100.0%; Pred. No. 9.4e-11;
tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                 CURPUTER: 14M FC COMPATIDATE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,871
FILING DATE: 19920103
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US/07/816,289
FILING DATE: 03 JAN 1992
PRIOR APPLICATION NUMBER: US/07/635,544
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US/07/635,544
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US/07/635,544
FILING DATE: 13-JUL-1989
PRIOR APPLICATION NUMBER: US/07/224,035
FILING DATE: 13-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: CINDBATE: 13-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: CINDBATA NUMBER: US/07/224,035
FILING DATE: 13-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: CINDBATA NUMBER: US/07/224,035
                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.2830004
TELECOMMUTCATION INFORMATION:
TELEPHONE: (202)833-9533
TELEFAX: (202)833-8716
                                                                                                                   COUNTRY: CZIP: 20036
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AMPUTER: IBM PC compatible
CAMPUTER: IBM PC COMPATIBLE
CAMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 32
US-08-351-149-4/c
; Sequence 4, Application US/08351149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGHT: 17327 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 100.(
Matches 52; Conservative
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16397..17327
        NUMBER OF SEQUENCES: 18
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9597..9744
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754..9596
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                                                                                     Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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COCATION:
US-07-906-871-15
                                                                                                    STATE: D
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HEMATOPOIETIC CELL SPECIFIC
TRANSCRIPTIONAL REGULATORY ELEMENTS OF SERGLYCIN AND USES
THEREOF
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                                                              9016 aatttttgtatttttagtagagatggggtttcaccatgttggccaggctggt 9067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 1776;
                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                   Sequence 12, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence TITLE OF INVENTION: Polypeptides and Methods of Use NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 72. CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: An Diego
CITY: San Diego
STATE: California
Best Local Similarity 100.0%; Pred. No. 1.2e-10; Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.2%; Score 52; DB 4; L 100.0%; Pred. No. 1.2e-10; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-LJ 2626
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Patent No. 5340739
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Avraham, Shalom
TITLE OF INVENTION: HERMATOPOIETIC C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFCATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-901
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.2%
Best Local Similarity 100.0
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36..1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                               RESULT 30
US-09-041-886-12/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-906-871-15/C
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US-09-041-886-12
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APPLICANT: Nicola, Nicos A.
APPLICANT: Gough, Nicholas M.
APPLICANT: Gough, Nicholas M.
APPLICANT: Gough, Nicholas M.
APPLICANT: Matcalf, Donald
APPLICANT: Ming, Julie Ann
TITLE OF INVENTION: Improvements in Granulocyte-Macrophage
TITLE OF INVENTION: Colony-Stimulating Factor Receptor and Derivatives Thereof
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                    SOFTWARTS STATEMENT OF THE CONTROL OF STATEMENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,828
FILING DATE: 07-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/351,149
FILING DATE: 23-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: FOX, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1256.0030001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Le
2.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.2%; Score 51; DB Best Local Similarity 100.0%; Pred. No. 2.5 Matches 51; Conservative 0; Mismatches
                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-895-474-4/c; Sequence 4, Application US/08895474; Patent No. 6136957; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1808 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC COM
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
150..1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
    Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                               U.S.A.
                                                               20002
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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US-08-384-828-4
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                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                        APPLICANT: Gough, Nicholas M.
APPLICANT: Gearing, David P.
APPLICANT: Metcalf, Donald
APPLICANT: Ming, Julie Ann
TITLE OF INVENTION: Colony-Stimulating Factor Receptor and Derivatives Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nicola, Nicos A.
APPLICANT: Gough, Nicholas M.
APPLICANT: Gearing, David P.
APPLICANT: Gearing, David P.
APPLICANT: King, Julie Ann
TITLE OF INVENTION: Improvements in Granulocyte-Macrophage
TITLE OF INVENTION: Colony-Stimulating Factor Receptor and Derivatives Thereof
CORRESPONDENCE ADDRESS:
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0.2%; Score 51; DB 1; Length 1808;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,149
FILING DATE: 23-NOV-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                     ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: FOX, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1256.0030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08384828
Patent No. 5726036
GENERAL INFORMATION:
                                               Nicola, Nicos A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1808 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150..1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                       20005
Patent No. 5629283
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                COUNTRY: U cZID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-08-351-149-4
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us-09-434-382-28.oli.rni

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APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
NUMBER OF SEQUENCES: 94
CORRESPONDERGE Moodcock, Washburn, Kurtz, Mackiewitz &
ADBRESSEE: No. 6040140ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 4709 gctaattttttgtatttttagtagagacggggtttcaccatgttggccagg 4759
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                                                                                                                                                                                                                                                                                                                   '' DB 2; Leus
''o. 2.8e-10; Indels
                                                                                                                                                                                                                                                                                                                                      Length 2559;
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SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: US/08/545,860D
FILING APPLICATION THE-1996
CLASSIFICATION TATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994
PRIOR APPLICATION NUMBER: PCT/US92/10930
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/327,392
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/327,392
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/327,392
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      0.2%; Score 51; DB 100.0%; Pred. No. 2.8 itive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,094
FILING DATE: 30-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,839
FILING DATE: 27-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-OCT-1994
PRIOR PAPLICATION DATA: US 08/062,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 36
US-08-545-860D-63/c
; Sequence 63, Application US/08545860D
; Patent No. 6040140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1993
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2559 base pairs
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.C
Matches 51, Conservative
                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: HUMAN
                                                                                                                                                                                                                           CDS.
216..1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                   FEATURE:

NAME/KEY:

LOCATION:

US-08-886-152-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 175.S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PLATELET ACTIVATING FACTOR
TITLE OF INVENTION: ACETYLHYDROLASE, AND GENE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin 1.20/m.20. Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,152 FILING DATE: 30-JUN-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.2%; Score 51; DB 3; Lr
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                           TELECOMMUNICATION INDICES
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFACK: (202) 371-2600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1808 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA.

APPLICATION NUMBER: JP 8-188369
FILING DATE: 28-JUN-1996
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-041-0
TELECOMONICATION INFORMATION:
TELEPHONE: 703-413-3000
US/08/895,474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-886-152-4/c
Sequence 4, Application US/0886152
Patent No. 5880273
GENERAL INFORMATION:
APPLICANT: ADACHI, HIDEKI
APPLICANT: TSUJINOTO, MASAFUMI
APPLICANT: TRIJINOTO, MASAFUMI
APPLICANT: ARAI, HIROYUKI
APPLICANT: INOUE, KEIZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                  FILING DATE: 16-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAMUEL L.
REGISTRATION NUMBER: 30,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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150..1349
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CORRESPONDENCE ADDRESS:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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TELEFAX: 7
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY;
; LOCATION;
US-08-895-474-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: A
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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Qy 10565 tgatccgcctgccttggcctcccaaagtgctgggattacaggcgtgagcca 10615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.2%; Score 51; DB 5; Length 8342; Best Local Similarity 100.0%; Pred. No. 2.4e-10; Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Rowley, Janet D.
APPLICANT: Diaz, Manuel O.
APPLICANT: Diaz, Manuel O.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DETECTING GENE REARRANGEMENTS AND TITLE OF INVENTION: TRANSLOCATIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ADD
                                           Patentin Release #1.0, Version #1.25
                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
                                                                                                                                                                                                                                                                                 TJU-1242
               OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1
TELECHMUNICATION INFORMATION:
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACPERISTICS:
LENGTH: 8342 base pairs
TYPE: NUCLEIC acid
STRANDEDMESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-080-255-6/c; Sequence 6, Application US/08080255; Patent No. 5487970
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3032..3145
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2353..2484
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8304..8342
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6788..6934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
595..666
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                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
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LOCATION:
FEATURE:
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LOCATION:
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NAME/KEY:
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LOCATION:
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FEATURE:
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NAME/KEY:
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Sequence 63, Application PC/TUS9404496
Sequence 63, Application PC/TUS9404496
Sequence 63, Application:
APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz &
ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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100.0%; Pred. No. 2.4e-10;
tive 0; Mismatches 0; Indels
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/805,093
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca ESq., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUT-1262
FELECOMMUNICATION INFORMATION:
FELEPHONE: (215) 568-3190
TELEFAX: (215) 568-3190
TELEFAX: (215) 568-3190
TELERAX: (215) 568-3100
TELERAY: (215) 568-3100
TELEGIT: 8342 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
AMMY COUNTY NONA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 100.0
Matches 51; Conservative
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7967..8062
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6788..6934
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8304..8342
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COUNTRY: USA
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595..666
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CITY: Philadelphia
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2..265
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US-08-545-860D-63
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LOCATION:
FEATURE:
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LOCATION:
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LOCATION:
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STATE:
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Sequence 6, Application PC/TUS9305857

Sequence 6, Application PC/TUS9305857

SPECIANT: Board of Regents

APPLICANT: The University of Texas System

APPLICANT: The University of Texas System

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING

TITLE OF INVENTION: GENE REARRANGEMENTS AND TRANSLOCATIONS
                                                                                                                                                                                                                                        Query Match 0.2%; Score 51; DB 3; Length 8392; Best Local Similarity 100.0%; Pred. No. 2.4e-10; Matches 51; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.4e-10;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:072/PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US93/05857
FILING DATE: 19930617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01/900,689
                           LENGTH: 8392 base pairs;
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-465-713-6
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TELEPHONE: (512) 320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: DNA (genomic)
PCT-US93-05857-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/90
FILING DATE: 17/06/92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Best Local Similarity 100.
Matches 51; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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APPLICANT: Diaz, Manuel O.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TRANSLOCATIONS
TITLE OF INVENTION: TRANSLOCATIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALNOId, White & Durkee
STREET: P. O. Box 4433
COUNTRY: Houston
STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/080,255
FILING DATE: 19930617
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PATEC, David G.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 32,165
TELEPHONE: (512) 320-720
TELEPHONE: (512) A74-757
SUPPROMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 8392 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER FALSABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,713
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PROOR APPLICATION NUMBER: US/08/080,255
FILING DATE: 17 JUNE 1993
ATTONNEY/AGENT INFORMATION:
NAME: ADELICATION NUMBER: US/08/080,255
FILING DATE: 17 JUNE 1993
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.2%; Score 51; DB 1; La
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 51; Conservative 0; Mismatches 0;
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REGISTRATION NUMBER: 32,165
REFREENCELPOCKET NUMBER: ARCD:072/PAR
TELECOMUNICATION:
TELEPHONE: (512) 330-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-465-713-6/c; Sequence 6. Application US/08465713; Patent No. 6121419; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (genomic) US-08-080-255-6
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TELEFAX: (512) 474-7577
INFORMATION FOR SPO ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER FILING DATE: 1998-04
EARLIER FILING DATE: 1998-04
EARLIER FILING DATE: 1997-08-04
NUMBER: OF SEQ ID NOS: 18
SOFTWARE: FASTER OF WINDOWS Version 3.0
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                   APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 03404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT PILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER PILING DATE: 1998-07-02
EARLIER PILING DATE: 1998-07-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTERQ for Windows Version 3.0
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Pred. No. 4.2e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.2%; Score 50; DB Best Local Similarity 100.0%; Pred. No. 4.2 Matches 50; Conservative 0; Mismatches
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US-08-724-394A-20
; Sequence 20, Application US/08724394A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/09128155 Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COCATION: (1)...(152331)
COTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
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; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                               SEQ ID NO 16
LENGTH: 152331
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                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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            Sequence 3, Application US/08618100B
Patent No. 6068976
GENERAL INFORMATION:
APPLICANT: Briggs, Michael R.
APPLICANT: Auwerx, Johan
APPLICANT: Staels, Bart
APPLICANT: Croston, Glenn E.
APPLICANT: Croston, Glenn E.
APPLICANT: Miller, Stephen G.
TITLE OF INVENTION: MODULATORS OF OB GENE AND
TITLE OF INVENTION: SCREENING METHODS THEREFOR
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
Sequence between exon 1 and exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: stcrage
COMPUTER: stcrage
COMPUTER: stcrage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,100B
FILING DATE: March 19, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/558,588
FILING DATE: ADJUST 2, 1995
APPLICATION NUMBER: 08/510,584
FILING DATE: ADJUST 2, 1995
APPLICATION NUMBER: 08/418,096
FILING DATE: ADJUST 2, 1995
APPLICATION NUMBER: 08/418,096
FILING DATE: ADJUST 2, 1995
APPLICATION NUMBER: 08/418,096
FILING DATE: MATCH 20, 1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                SCREENING METHODS THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 42
US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 611/654
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : (213) 489-1600
(213) 955-0440
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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US-08-618-100B-3
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US-08-618-100B-3/c
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COUNTRY:
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Length 246240;
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APPLICANT: Feder, John N.
APPLICANT: Feder M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TTILE OF INVENTION: Agebase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.2%; Score 50; DB 2; Length 246 Best Local Similarity 100.0%; Pred. No. 4e-10; Matches 50; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: U1-0CT-1996
CLASSIFICATION: 536
ATTONREY/AGENT INPORMATION:
NAME: Fitts, Renee A:
REGISTRATION NUMBER: 35,136
REFRENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 21:
SEQUENCE CHRACTERISTICS:
LENTH: 246240 base pairs
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                 SEE: TOWNSEND and TOWNSEND and CREW LLP : Two Embarcadero Center, 8th Floor San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: not relevant
TOPOLOGY: not relevant
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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STATE: CA
COUNTRY: USA
TTO: 94111-3834
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                                                                                                       COUNTRY: USA
ZIP: 94111-3834
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                                                              CITY: S
STATE:
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APPLICANT: Feder, John N.
APPLICANT: Feder, Peter M.
APPLICANT: Lauer, Peter M.
APPLICANT: Thomas, Minston
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ELOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                           STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  017957-000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JARANUEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: CDNA
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INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
TRNGTH: 246240 base pairs
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LOCATION: 1..246240
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Best Local Similarity
Matches 50; Conserv
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Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                        CA
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STATE:
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REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 9278 base pairs
                                                                                                                                                                                                                                                                                                                                                                            human DNA cosmid library
REGISTRATION NUMBER: 32 549
                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
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1081..1156
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1725..1792
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2588..2754
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3445..3535
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3645..3696
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4014..4113
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4920..5000
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5347..5397
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4196..4267
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2182..2256
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2339..2410
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5767..5866
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308..374
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909..994
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FEATURE:
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0.2%; Score 50; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 4e-10;
Matches 50; Conservative 0; Mismatches 0; Indels 0
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| Sequence 9, Application US/08243542
| Patent No. 555256
| GENERAL INFORMATION:
| APPLICANT: NAKAWURA, YUSUKE
| APPLICANT: NEWLY MITSURU
| TITLE OF INVENTION: ENCODING THE SAME
| TITLE OF INVENTION: ENCODING THE SAME
| NUMBER OF SEQUENCES: 20
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C. STREET: 2026 Rambling Road
| CITY: Ralamazoo STATE: Michigan
| COUNTRY: USA MICHIGAN
| COUNTRY: USA MICHIGAN
| MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage COMPUTER: IBM PC/XT/AT Compatible
| COMPUTER: IBM PC/XT/AT Compatible
| COMPUTER: IBM PC/XT/AT Compatible
| COMPUTER: NOT COMPATED STREET: MICHIGAN STREE
                                                                                ATTORNEY AGENT INFORMATION:
NAME: Fitts, Renee A.
NAME: Fitts, Renee A.
RECISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHOME: 415-576-0200
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
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FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
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APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY AGENT INFORWATION:
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CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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FILING DATE: 12 AP
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LIBRARY: human DNA cosmid library
                  TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 9278 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
    TELECOMMUNICATION INFORMATION:
                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: 2126 Rambling Road
CITY: Ralamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette, 3.5 inches, 1.44 Mb storage
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette, 3.5 inches, 00PPUTER: IBM PC/XT/AT Compatible
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 48
US-08-477-407-9/C
US-08-477-407-9/C
Sequence 9, Application US/08477407
Patent No. 5631351
GENERAL INFORMATION:
APPLICANT: NARAMURA, YUSUKE
APPLICANT: BMI, MITSURU
ITLE OF INVENTION: EMC PROTEINS AND DNAS
TITLE OF INVENTION: EMC PROTEINS AND DNAS
TITLE OF INVENTION: EMCOBING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
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CLASSIFICATION NOMBER: 05/01/195
CLASSIFICATION DATE: 05/01/195
PRIOR APPLICATION DATE: 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-49904
FILING DATE: 12 APRIL 1994
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FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
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8165..9038
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6073..6202
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; LOCATION:
US-08-243-542-9
                                               FEATURE:
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TELEFAX: (616) 381-5465

INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 9278 base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human DNA cosmid library
ENTURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2026 Kampling Koad
CITY: Kalamazoo
CITY: Kalamazoo
COUNTRY: USA
ZIP: 49000-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,355
FILING DATE: 07-JUN-1995
CLASSIPICATION NUMBER: US 08/243,542
FILING DATE: 13-MX-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 12 SEPERBER: JP 5-257455
FILING DATE: 22 SEPERBER: JP 6-4904
FILING DATE: 22 SEPERBER: JP 6-4904
FILING DATE: 22 SEPERBER: JP 6-4904
FILING DATE: 23 SEPERBER: JP 6-4904
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FILING DATE: 27 SEPERBER: JP 6-4904
FILING DATE: 27 SEPERBER: JP 6-4904
FILING DATE: 23 SEPERBER: JP 6-4904
FILING DATE: 37 SEPERBER: JP 6-4904
FILING DATE: 37 SEPERBER: JP 6-4904
FILING DATE: 37 SEPERBER: JP 6-4904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08484355
| Patent No. 5705341
| GENERAL INFORMATION:
| APPLICANT: NAKAMURA, YUSUKE |
| APPLICANT: NAKAMURA, YUSUKE |
| TITLE OF INVENTION: MDC PROTEINS AND DNAS |
| TITLE OF INVENTION: ENCODING THE SAME |
| NUMBER OF SEQUENCES: 20 |
| CORRESPONDENCE ADDRESS: ADDRESSE: FLYNN, THIEL, BOUTELL & TANIS P.C. |
| STREET: 2026 Rambling Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
RETERENCE/POCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
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FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
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; LOCATION:
US-08-477-407-9
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GENERAL INFORMATION:
APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
APPLICANT: Fair, William R.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Israeli, Ron S.
APPLICANT: Hescon, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2957;
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125 TTTTTAGTAGAGACGGGTTTCACCATGTTGGCCAGGCTGGTTGAA 78
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:

ZIP: 10036
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 Dx2
COMPUTER: IBM 330 466 Dx2
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
REFERENCE/DOCKET NUMBER: 4446-B
TELEPHONE: (212) 279-0525
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENTH: 2957 base pairs
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100.0%; Pred. No. 3.7e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | IMMEDIATE SOURCE:
| CLONE: Prostate Specific Membrane Antigen
US-08-394-152A-48
                                                                                                                                                                                                                                                                                                         E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: United States of America
                                                                                                              Sequence 48, Application US/08394152A Patent No. 5935818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39, Application US/08394152A Patent No. 5935818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 0.2
Best Local Similarity 100.
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE TYPE:
                                                                                              US-08-394-152A-48/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-394-152A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                Oy 11137 titttagtagagacggggtttcaccatgttggccaggctggtcttgaa 11184
                                                                                                                                                                                                                                                                                                                           Length 9278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 282;
                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-133-629-8/C
Sequence 8, Application US/08133629
Patent No. 5597694
GENERAL INFORMATION:
APPLICANT: Munroe, David J.
APPLICANT: HOUSMAN, DAVID E.
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.9e-09;
hes 0;
                                                                                                                                                                                                                                                                                                                           DB 1; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.2%; Score 48; DB 1; Best Local Similarity 100.0%; Pred. No. 4.9e-0 Matches 48; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Wolf, Greenfield & Sacks, P.C STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                       Query Match 0.2%; Score 49; DB Best Local Similarity 100.0%; Pred. No. 1.4 Matches 49; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Greer, Helen
REGISTRATION NUMBER: 36,816
REFERENCE/DOCKET NUMBER: M0828/7001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/133,629
FILING DATE: 07-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 92-1742 EZEKIEL INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 282 base pairs
TYPE: nucleic acid
exon 21
6300..6468
                                                                                                                                                                     exon 24
7829..7846
                                                                                                                                                                                                                          exon 25
8165..9038
                                                       exon 22
6557..6671
                                                                                                              exon 23
6756..6846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02210
                                                   NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                              NAME/KEY:
NAME/KEY:
                   LOCATION:
                                                                                                                                                                                                                                              . LOCATION:
US-08-484-355-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-133-629-8
                                   FEATURE:
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Gaps

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APPLICANT: Takanori OKURA
APPLICANT: Takanori OKURA
APPLICANT: Masahi TORIGOE
APPLICANT: Masahi KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.2%; Score 48; DB 1; Le Best Local Similarity 100.0%; Pred. No. 3.4e-09; Matches 48; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D. C.
COUNTRY: USA
                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/821,415
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH001.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTOMERY/ABOTET INFORMATION:
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-884-324-10/c
; Sequence 10, Application US/08884324
Patent No. 6060283
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 6340 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
CLONE: PCNA Genomic Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                      CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-187-785-3
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Patent No. 5756476
GENERAL INFORMATION:
APPLICANT: Epstein, Stephen
APPLICANT: Spelr, Edith
TITLE OF INVENTION: Inhibition of No. 5756476-Transformed Cell
TITLE OF INVENTION: Proliferation Using Anti-Sense Oligonucleotides
NUMBER OF SEQUENCES:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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100.0%; Pred. No. 3.7e-09;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: United States of America
21P: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX.
COMPUTER: IBM 330 466 DX.
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION: UNDERFY: 28,678
REGISTRATION UNDERFY: 28,678
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | IMMEDIATE SOURCE:
| CLONE: Prostate Specific Membrane Antigen
US-08-394-152A-39
                                                               E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE DOCKET NUMBER: 41426-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHRACTERISTICS:
LENGTH: 3017 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.29
Best Local Similarity 100.4
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapien
TISSUE TYPE: Carcinom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide HYPOTHETICAL: NO
                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92660
                                                            ADDRESSEE:
STREET: 11
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US-08-187-785-3/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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REFERENCE/DOCKET NUMBER: OKURA=1

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                           0.2%; Score 48; DB 1; Length 20303;
ilarity 100.0%; Pred. No. 3e-09;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9015 taatttttgtattttagtagagatggggtttcaccatgttggccagg 9062
                                                                                                                               9428 TAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGG 9381
                                                                                                                                                                                                                                                                                                           APPLICANT: Maley, Frank
APPLICANT: Maley, Gladys F.
APPLICANT: Maley, Gladys F.
APPLICANT: Welley, Bladys F.
TITLE OF INVENTION: Human Deoxycytidylate Deaminase Gene
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER LOSA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/370,975B

FLING DATE: 10-JAN-1995

CLASSIFICATION: 435

ATTORNEY APERIT INFORMATION:

NAME: Timian, Susan J.

REGISTRATION NUMBER: 20894/80

TELEPONE: (716,263-1600)

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 26764 base pairs

TYPE: nuclaic acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Nixon, Hargrave, Devans & Doyle Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 57
US-08-884-324-14/C
Sequence 14, Application US/08884324
Fatent No. 6060283
GENERAL INFORMATION:
APPLICANT: Takanori OKURA
APPLICANT: Rakuji TORIGOE
APPLICANT: Masahi KURIMOTO
                                                                                                                                                                                                                           US-08-370-975B-1/c
; Sequence 1, Application US/08370975B
; Patent No. 5622851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CHROMOSOME/SEGMENT: 4q35
US-08-370-975B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.2
Best Local Similarity 100.
Matches 48; Conservative
                                           Best Local Similarity
Matches 48; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Clinton
CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                         0.2%; Score 48; DB 3; Length 8835; 100.0%; Pred. No. 3.3e-09; tive 0; Mismatches 0; Indels ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Maley, Frank
APPLICANT: Maley, Gladys F.
APPLICANT: Weiner, Karen X.B.
TITLE OF INVENTION: Human Deoxycytidylate Deaminase Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester . STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20894/80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 2089
TELECOMMUNICATION INFORMATION:
TELEFRANCE (716)263-1636
TELEFRANCE (716)263-1636
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 8835 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHROMOSOME/SEGMENT: 4q35
                                                                                                                                                                                                                                                                                                                                                                                                                                                   48; Conservative
                                                                                                                                                                                                                                                                                      NAME/KEY: intron
COCATION: 1..8835
DENTIFICATION METHOD:
US-08-884-324-10
                                                                                                                                                                                                                                                TISSUE TYPE: placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 48; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 55
US-08-370-975B-6/c
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NAME/KEY: 3'UTR
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GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE OF INDUCING THE PRODUCTION OF INTERFERON-35
                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
COMPUTER: IBM PC COMpatible
COMPUTER: TARENT PC PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE: CLASSIFICATION A135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                         ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OKURA-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTONANE: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKUR.
TELECOMMUNICATION IFFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 28994 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: intron
LOCATION: 15686..17056
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 17057..17068
IDENTIFICATION METHOD: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: leader peptide LOCATION: 15607..15685 IDENTIFICATION METHOD: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..15606
IDENTIFICATION METHOD: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leader peptide 20452..20468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 20587..21920
IDENTIFICATION METHOD: ENAME/KEY: mat peptide
LOCATION: 21921..22054
IDENTIFICATION METHOD: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: intron
LOCATION: 17069..20451
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: mat peptide COCATION: 20469..20586 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat peptide
26828..27046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22055..26827
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TITLE OF INVENTION: GE
TITLE OF INVENTION: OF
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: 5'UTR
                                                                                                                                                                               20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                     STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schuchman, Edward H.
APPLICANT: Desnick, Robert J.
TITLE OF INVENTION: Acid Sphingomyelinase Gene and Diagnosis
TITLE OF INVENTION: of Niemann-Pick Disease
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                      Length 28994;
                                                                                                                                                              Length 1664;
                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,740
FILING DATE: 27-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.2%; Score 46; DB 1; Le
100.0%; Pred. No. 2.3e-08;
tive 0; Mismatches 0;
                                                                                      0.2%; Score 48; DB 3; L4
100.0%; Pred. No. 2.9e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6923-038
                                                                                                                                                                                                                                                                                           Sequence 34, Application US/08250740 Patent No. 5686240 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-695-472B-3
; Sequence 3, Application US/07695472B
; Patent No. 5773278
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGIESTRATION NUMBER: 30742
REFRENCE/COCKET NUMBER: 692:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1664 base pairs
                                                                                  Query Match 0.28
Best Local Similarity 100.0
Matches 48; Conservative
; LOCATION: 27047..28994
; IDENTIFICATION METHOD:
US-08-884-324-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
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Best Local Similarity
Matches 46; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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US-08-250-740-34
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RESULT 61
US-08-687-080-55/C
Sequence 55, Application US/08687080
Fatent No. 5965427
GENERAL IMPORMATION:
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CORTY: Palo Alto
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                   Length 1926;
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                                                                                                                                                                  Indels
                                                                                                                                                                                                               8388 aggccgggtgcagtggctcacgcctgtaatcccagcactttgggag 8433
                                                                                                                                                                                                                                       5' END OF RAD50 GENOMIC SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94300

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION NUMBER: US/08/592,126
FILING DATE: 26-JAN-1996
APPLICATION NUMBER: US 08/592,126
FILING DATE: 18-JAN-1996
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELEPHONE: (415) 324-0880
TELEFAMICATION NUMBER: 4600-0111.30
TELEFAMICATION NUMBER: 4600-0111.30
TELEFAMICATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELEFAMICATION NUMBER: 24-0860
TELEFAMICATION NUMBER: 24-0860
TELEFAMICATION NUMBER: 2600-0111.30
TELEFAMICATION NUMBER: 304-0860
TELEFAMICATION NUMBER: A600-0111.30
TELEFAMICATION NUMBER: A600-0111.30
TELEFAMICATION NUMBER: A600-0111.30
TELEFAMICATION NUMBER: A600-0111.30
TELEFAMICATION SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 2886 base pairs
TYPE: NUCLEIC acid
STRNDEDNESS: double
                                                                                                                   Query Match 0.2%; Score 46; DB 4; Le Best Local Similarity 100.0%; Pred. No. 2.2e-08; Matches 46; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.2%
Best Local Similarity 100.1
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE:
US-08-687-080-55
; NAME/KEY: CDS
; LOCATION: (72)..(1553)
US-09-117-250-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: ·linear
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US-08-951-648-5/C
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APPLICANT: Rainmura, Tarka-aki
APPLICANT: Rishimoto, Toshihiko
APPLICANT: Makino, Yasutaka
APPLICANT: Makino, Yasutaka
TITLE OF INVENTION: METHOD OF DETECTING ANTI-DADII ANTIBODY AND METHOD OF
TITLE OF INVENTION: CANCER USING THE DETECTING METHOD
FILE REFERENCE: 7898/225192
CURRENT APPLICATION NUMBER: US/09/117,250A
CURRENT APPLICATION NUMBER: DP8-11695
EARLIER APPLICATION NUMBER: PP8-11695
EARLIER PILING DATE: 1996-01-26
SERLIER APPLICATION NUMBER: PCT/JP97/00174
EARLIER FILING DATE: 1997-01-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN, Version 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Desnick, Robert J.
TITLE OF INVENTION: The Acid Sphingomyelinase Gene and
TITLE OF INVENTION: Diagnosis of Niemann-Pick Disease
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/695,472B
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0.2%; Score 46; DB 1; Lv
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 46; Conservative 0; Mismatches 0;
                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6923-014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09117250A Patent No. 6251613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY FACETY INFORMATION:
NAME: Mistock, S. Leslie
REGISTATION UNBER: 18,923
REFERENCE/DOCKET UNBER: 6923
TELECOMUNICATION INFORMATION:
TELEFHONE: (212) 790864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1664 base pairs
  Schuchman, Edward H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  19910503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 199105
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEIC ACID
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ORGANISM: Homo.sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: CDNA
US-07-695-472B-3
                                                                                                                                                                                                          3: New York
PRY: U.S.A.
10036
                                                                                                                                                                                                               STATE: NE
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 4
LENGTH: 1926
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US-08-250-740-35
Sequence 35, Application US/08250740
Patent No. 5686240
GENERAL INFORMATION:
APPLICANT: Schuchman, Edward H.
APPLICANT: Desnick, Robert U.
TITLE OF INVENTION: Acid Sphingomyelinase Gene and Diagnosis TITLE OF INVENTION: of Niemann-Pick Disease
                                                   Length 3195;
                                                                                                                                       Sequence 4, Application US/07695472B
Patent No. 5773278
GENERAL INFORMATION:
APPLICANT: Schuchman, Edward H.
APPLICANT: Desnick, Robert J.
TITLE OF INVENTION: The Acid Sphingomyelinase Gene and
TITLE OF INVENTION: Diagnosis of Niemann-Pick Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/695,472B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.2%; Score 46; DB 1; Le Best Local Similarity 100.0%; Pred. No. 2e-08; Matches 46; Conservative 0; Mismatches 0;
                                                   Query Match 0.2%; Score 46; DB 3; L. Best Local Similarity 100.0%; Pred. No. 2.1e-08; Matches 46; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INPORMATION:
NAME: Misrock, S. Leslie
REGISTATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6923:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 790-864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-07-695-472B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 4741 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19910503
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                                                                                                                             US-07-695-472B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3195;
                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker, Sears Tower Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.2%; Score 46; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 46; Conservative 0; Mismatches 0;
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APPLICANT: Loughney, Kate
TITLE OF INVENTION: Phosphodiesterase 8A
TITLE REFERENCE: 27866/35047
CURRENT APPLICATION NUMBER: US/09/174,437A
CURRENT FILING DATE: 1998-10-16
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: 9195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: WAILIAMS JI., JOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/34038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAN: 312-474-6448
                                                                      APPLICANT: Loughney, Kate
TITLE OF INVENTION: Phosphodiesterase
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/951,648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09174437A Patent No. 6133007
Sequence 5, Application US/08951648 Patent No. 5932465 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 3195 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67..2403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (67)..(2403)
US-09-174-437-5
                                                                                                                                                                               STREET: 233 South CITY: Chicago STATE: Illinois COUNTRY: US ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-08-951-648-5
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APPLICANT: RIEFER, MICHAEL C.
APPLICANT: BARR, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.2%; Score 46; DB 1; Length 5408; 100.0%; Pred. No. 2e-08; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9015 taatttttgtatttttagtagagatggggtttcaccatgttggcca 9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4880 TAATTTTTGTATTTTAGTAGAGATGGGGTTTCACCATGTTGGCCA 4835
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IIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                  23647-20007.12
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FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/471,05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08/320,157
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,15
FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHHHARDY, SUSAN K.
REGISTRATION NUMBER: 33,943
REPERRINCE/DOCKET NUMBER: 2364
TELECOMMUNICATION INFORMATION:
TELEDRONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 494-0792
TELEEX: 706141
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARATERISTICS: LENGTH: 5408 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Coding Sequence LOCATION: 1665...1928
CTHER INFORMATION:
US-08-471-058-20
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Best Local Similarity 100.(
Matches 46; Conservative
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Sequence 20, Application US/08471058

Patent No. 5770443

Patent No. 5770443

GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
APPLICANT: Riefer, Philip J.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CORRESPONDENCES: 24

CORRESPONDENCE ADDRESS:
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Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 46; Conservative 0; Mismatches 0;
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SOFTWARE: Fast-EDO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/250,740
FILING DATE: 27-MAY-1994
CLASSIPICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 6923-038
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: DNA (genomic) US-08-250-740-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                     STATE: New York COUNTRY: USA
                                                                                                                                                                   10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75431 AGCCCGGGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAG 75386
                         8388 aggccgggtgcagtggctcacgcctgtaatcccagcactttgggag 8433
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                                                                                                                                                                                                                                                                                 APPLICANT: Laver, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SOURNESS: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. No. 1.3e-08; tive 0; Mismatches 0;
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; OTHER INFORMATION: /note- "HLA-H.CONFIG"
US-08-724-394A-21
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US-08-724-394A-22/C
; Sequence 22, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
                                                                                                                                                                            Sequence 21, Application US/08724394A Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 3.30
ATTORNEY/AGENT INFORMATION:
NAME: FILTS, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-020
TELEPHONE: 415-576-020
: INFORMATION FOR SED ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIA
                                                                                                                                                                                                                                                                   APPLICANT: Kronmal, Gregory S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS: not relevant not relevant
                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100. Matches 46; Conservative
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TYPE: nucleic acid
STRANDEDNESS: not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: not rely
MOLECULE TYPE: CDNA
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Feder, John N.
APPLICANT: Kromal, Gregory S.
APPLICANT: Kromal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Trauchihashi, Zenta
APPLICANT: Trauchihashi, Zenta
APPLICANT: Trauchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: TWO Embarcadero Center, 8th Floor
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                                                                                                                                                                                               Length 5408;
                                                                                                                                                                                          Ouery Match 0.2%; Score 46; DB 3; Length 540 Best Local Similarity 100.0%; Pred. No. 2e-08; Matches 46; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      017957-000100
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; Sequence 20, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A
REGISTRATION NUMBER: 35,136
REFREENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 246240 base pairs
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Best Local Similarity 100°
Matches 46; Conservative
                                                                                                        1665..1928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
TYPE: nucleic acid STRANDEDNESS: sing]
                                           TOPOLOGY: linear
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                                                                                      NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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US-08-471-057-20
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STATE:
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210121.439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                    double
                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NAMNI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                           No. 5872237el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 75431 AGGCCGGGTGCAGTGCCTCACGCCTGTAATCCCAGCACTTTGGGAG 75386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8388 aggccgggtgcagtggctcacgcctgtaatcccagcactttgggag 8433
  APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
Annupreper Corresponder Contraction
                                                                                                                                                                                                                                                                                       COUNTY: USA

ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
ATTORKEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET UNMBER: 35,136
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET UNMBER: 35,2000
TELEPHONE: 415-576-0200
TELEPHONE: 415-576-0200
INFORMATION FOR SEO ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 22640 base pairs
                                                                                                                                                              STREET: TWO EMDARCAGES AND TOWNSEND AND CREW LLP STREET: TWO Embarcadero Center, 8th Floor CIIY: San Francisco STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.2%; Score 46; DB 2; Ls Best Local Similarity 100.0%; Pred. No. 1.3e-08; Matches 46; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 76, Application US/08687080
Patent No. 5965427
GENERAL INFORMATION:
APPLICANT: GENEORY Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Met
CORRESPONDENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22
Kronmal, Gregory S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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TREATM
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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) INDIVIDUAL ISOLATE: INTRON 9 OF RAD50 GENOMIC SEQUENCE
US-08-687-080-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 17-JUL-1996
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: 08/592,126
FILING APPLICATION NUMBER: 08/592,126
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRERENCE/DOCKET NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELEDOMMUNICATION INFORMATION:
TELEDOMMUNICATION:
TELEDOMMUNIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEAD PC COMPUTER:
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,762
FILING DATE: 21-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MARKI, DAVIG J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.2%; Score 45; DB 2; La
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 45; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:

APPLICANT: Goldstein, Gideon
APPLICANT: Culler, Michael
TITLE OF INVENTION: Method for the Diagnosis of Depression
TITLE OF INVENTION: Based on Monitoring Blood Levels of Arginine Vasopressin
TITLE OF INVENTION: and/or Thymopoietin
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: 321 No. 5591588ristown Road, Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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10503 tttttttagtagagacggggtttcaccatgttggccaggatggtc 10547
                       2383 TITITITAGIAGAGGGGGTTTCACCATGTTGGCCAGGATGGTC 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08309419
Patent No. 5593842
GENERAL INFORMATION:
APPLICANT: Goldstein, Gideon
APPLICANT: Culler, Michael
TITLE OF INVENTION: Method of Measuring Thymopoietin
TITLE OF INVENTION: Proteins in Plasma and Serum
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWSON and HOWSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 1; I
Pred. No. 5.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.2%; Score 45; DB ilarity 100.0%; Pred. No. 5.2 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BAK, MARY E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR146
TELECOMMUNICATION: TELECOMMUNICATION: (215) 540-9207
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 2392 base pairs
                                                                                                                                                        Sequence 5, Application US/08309420 Patent No. 5591588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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241..1275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: PR
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
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                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Setcavage, Diane R.
TITLE OF INVENTION: Recombinant Human Thymopoietin Proteins
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STRRET: Spring House Corporate Cutr, P.O. Box 457
CITY: Spring House
STRATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.2%; Score 45; DB 1; Length 2392; Best Local Similarity 100.0%; Pred. No. 5.2e-08; Matches 45; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                  Length 2373;
                                                                                                                                                                                                                                                                                                                1972 GGCCGGGTGCACGCCTCTAATCCCAGCACTTTGGGAG 2016
                                                                                                                                                                                                                                                                                      8389 ggccgggtgcagtggctcacgcctgtaatcccagcactttgggag 8433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/171,382
                                                                                                                                                                                                Query Match 0.2%; Score 45; DB 4; L. Best Local Similarity 100.0%; Pred. No. 5.3e-08; Matches 45; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUALLE CATE.

FILING DATE.

CLASSIFICATION: 514

ATTORNEY, AGENT INFORMATION:

NAME: BAK, MARY E.

REGISTRATION NUMBER: 31,215

REFERENCE, DOCKET NUMBER: IR143USA

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9206

""" FFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Talle, Mary Anne
APPLICANT: Shenbagamurthi, Ponniah
APPLICANT: Culler, Michael D.
APPLICANT: Setcavage, Diane R.
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 73
US-08-171-382-5/C
Sequence 5, Application US/08171382
Patent No. 5472856
GENERAL INFORMATION:
APPLICANT: Harris, Crafford A.
APPLICANT: Goldstein, Gideon
HAPLICANT: Siekierka, John J.
                                                                                                       ; MOLECULE TYPE: DNA (genomic) US-08-975-762-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2392 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                  LENGTH: 2373 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
241..1275
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-171-382-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                          Matches
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Gaps

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APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Method for the Diagnosis of
TITLE OF INVENTION: Depression Based on Monitoring Blood Levels of
TITLE OF INVENTION: Arginine Vasopressin and/or Thymopoietin
CORRESPONDENCES: 7
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                                                                                                                                                                                                                                                                                                                                                                     Length 2392;
                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                     DB 5; Le 5.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZUET 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version#1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11878
                                                                                                                                                                                                                                                                                                                                                                  0.2%; Score 45; DB 100.0%; Pred. No. 5.2 tive 0; Mismatches
REFERENCE/DOCKET NUMBER: IRI45BPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2392 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 321 Norristown Road, Box 457 CITY: Spring House COUNTY: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFRENCE/DOCKET NUMBER: IR146PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEPHONE: (215) 540-5818
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,420
FILING DATE: 20-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application PC/TUS9511878 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.4
Matches 45; Conservative
                                                                                                                                                                                                                                                               CDS
241..1275
                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 77
PCT-US95-11878-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
PCT-US95-11878-5
                                                                                                                                                                                                                                                             ) NAME/KEY:
) · LOCATION:
PCT-US95-11856-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                         FEATURE
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Sequence 5, Application PC/TUS9511856

GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Method of Measuring
TITLE OF INVENTION: Thymopoietin Proteins in Plasma and Serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.2%; Score 45; DB 1; Length 2392;
100.0%; Pred. No. 5.2e-08;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version#1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11856
  : 321 No. 5593842ristown Road, Box 457
Spring House
                                                                                                                                                                                                                                                    FILING DATE:

FILING DATE:

GLASSIFTCATION: 435
ATTONNEY, AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 1R145BUSA
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 540-9206
TELEPHONE: (215) 540-5818
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2392 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Howson and Howson
STREET: 321 Norristown Road, Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,419
FILING DATE: 20-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                     ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bak, Mary E.
REGIȘTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.2%
Best Local Similarity 100.0
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: CDS
; LOCATION: 241..1275
US-08-309-419-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: cDNA
                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΡA
                                                                  COUNTRY:
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Sequence 7, Application US/08757223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                         STREET: 2200
CITY: Dallas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 80
US-08-611-587-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                          APPLICANT: Hayden, Michael R.
APPLICANT: Hayden, Abigail
APPLICANT: Hay A.H.M. Mabbubl
APPLICANT: Hopra, Vikramjit Singh
APPLICANT: Chopra, Vikramjit Singh
APPLICANT: Ralchman, Michael
TITLE OF INVENTION: Apoptosis Modulators That Interact with the
TITLE OF INVENTION: Huntington's Disease Gene
NUMBER OF SEQUENCES: 44
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Oppedabl':
STRREW
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                                               Gaps
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             Length 2392;
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100.0%; Pred. No. 5e-08;
.ive 0; Mismatches 0; Indels
                                             0; Indels
                                                                      OTHER INFORMATION: exon 29 and partial cds of HIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 80443-5270
COMPUTER READABLE FORM:
WEDJUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS DOS 5.0
        DB 5; Le
5.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32038
REFERENCE/DOCKET NUMBER: UBC.P-013US2:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
TELEFAX: (970) 668-2050
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
             0.2%; Score 45; DB ilarity 100.0%; Pred. No. 5.2 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,199B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: genomic DNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: double
      Ouery Match
Best Local Similarity
Matches 45; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nc. stranbedness: dou
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ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                              Frisco
                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                      RESULT 78
US-09-085-199B-44/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-085-199B-44
                                                                                                                                                                                                                                                                                                                                                                                            STREET: FC CITY: FC STATE: CC COUNTRY:
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US-08-757-223-7/c

RESULT 79

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Gaps
Patent No. 6136530
GENERAL INFORMATION:
APPLICANT: Poduslo, Shirley E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ASSESSING RISK
TITLE OF INVENTION: FACTORS IN ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MONTERMINI, LAURA
APPLICANT: MONTERMINI, LAURA
APPLICANT: MOLTO, MARIA D.
APPLICANT: MOLTO, MARIA D.
APPLICANT: Campuzano, Victoria
APPLICANT: Cassee, Mireille
APPLICANT: Cossee, Mireille
ATITLE OF INVENTION: Direct Diagnosis of Friedreich Ataxia
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4588 ccaggctggagtgcagtggcatgatctcggctcactgcaacctcc 4632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Fulbright & Jaworski L.L.P. Patent Dept. 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                    STATE: CATAGES
ZIP: 75201-6776
COMPUTER READBLE FORM:
MEDIOW TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,223
FILING DATE: NO. 6136530ember 27, 1996
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.2%; Score 45; DB 3; L. 100.0%; Pred. No. 4.8e-08; iive 0; Mismatches 0;
                                                                                                                                                                               ADDRESSEE: Locke Purnell Rain Harrell
STREET: 2200 Ross Avenue, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/611,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08611587 Patent No. 6150091 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REFERENCE/DOCKET NUMBER: 4-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214/740-8785
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 5375 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 100.
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: single
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ADDRESSEE: Fulbright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Caskey, C. T.
APPLICANT: Fu, Ying-Hui
APPLICANT: Friedman, David L.
APPLICANT: Friedman, David L.
APPLICANT: Friedman, David L.
APPLICANT: Fenwick, Raymond G.
TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.2%; Score 45; DB 1; Length 11613; 100.0%; Pred. No. 4.4e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                          Length 8779;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                       Qy 4715 tttttgtatttttagtagagacggggtttcaccatgttggccagg 4759
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,044
FILING DATE:
                                                                                                                                                                                                                                          0.2%; Score 45; DB 2; L. 100.0%; Pred. No. 4.5e-08; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PLIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/019,940
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: D-5443
TELECHONE: 713/651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08484044 Patent No. 5552282 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: DNA (genomic)
US-08-484-044-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 11613 base pairs
                                                                              MOLECULE TYPE: genomic DNA
  LENGTH: 8779 base pairs
                                                                                                                                                                                                                                          Query Match 0.2
Best Local Similarity 100.
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.2
Best Local Similarity 100.
Matches 45; Conservative
                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double
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                                                                                                                    NAME/KEY: CYP2A13;
LOCATION:
CTHER INFORMATION:
US-08-750-703-4
                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1301 MCCITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-484-044-10/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.2%; Score 45; DB 3; L 100.0%; Pred. No. 4.6e-08; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08750703
Patent No. 5891633
GENERAL INFORMATION:
APPLICANT: GONZALEZ, FrANK J.; Idle, Jeffrey R.
TITLE OF INVENTION: DEFECTS IN DRUG
TITLE OF INVENTION: METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36,434
ER: 2026-4196PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATORNATOR DATE:
POTATOR DATE:
POTATOR DATE:
ATTORNEY/AGENT 16-JUN-1995
ATTORNEY/AGENT 11FORMATION:
NAME: DOZOCHY R. AUCH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET UNMBER: 2026-4196PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SED ID NO: 4:
SEQUENÇE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/750,703
                CLASSIFICATION: 436
ATTONREY/AGENT INFORMATION:
NAME: Brashears-Macatee, Sarah J.
REGISTRATION NUMBER: 38,087
                                                                                                 D-5901
                                                                                           REFERENCE/DOCKET NUMBER: D-59
TELECOMMUNICATION INFORMATION:
TELEPONE: 713-651-5620
TELERA: 713-651-546
TELEX: 76-2829
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8353 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Morgan & Finnegan
STREET: 345 Park Ave.
CITY: New York
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapien
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 9q13
03-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    linear
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ZIP: 10154-0053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; US-08-611-587-1
                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-750-703-4/c
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Sequence 11, Application US/09318448

Sequence 11, Application US/09318448

Patent No. 6210950

GENERAL INFORMATION:
APPLICANT: Stenroos, Edward S.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-67
CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 30500 No. 6025183thwestern Highway, Suite 410 CITY: Parmington Hills STATE: Mindigan COUNTRY: U.S.
ZIP: 48334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08814095
Patent No. 6025183
GENERAL INFORMATION:
APPLICANT: Sored, Hermona
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including ACHE
DESCRIPTION: promotor, ACHE gene and ARS gene"
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.2%; Score 45; DB 4; L. Best Local Similarity 100.0%; Pred. No. 4.2e-08; Matches 45; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MONTGOMETY, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 35060 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         double
                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-318-448-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                LENGTH: 18596
US-09-318-448-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-814-095-7
                                                                                                                                                                                                                                                                                             SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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              join(7540..7650, 9814..9945, 10421..10519, 11602..11787)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
OPERATURG SYSTEM: PC-DOS/AKS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,011
FILING DATE: 11-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
RAPLICATION DATA:
RAPLICATION NUMBER: US 08/047,246
FILING DATE: 13-APR-1993
                                                                                                                                                                                                                                       APPLICANT: ONDA, Haruo
APPLICANT: KIMURA, Chiharu
APPLICANT: KIMURA, Chiharu
APPLICANT: CHKUBO, Shoichi
TITLE OF INVENTION: NOVEL DNA AND USE THEREOF
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
ADDRESSEE: ROBERTS & CUSHMAN
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S
REGISTATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 41155-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-3400
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,676
FILING DATE: 07-AUG-1991
                                                                                                                                                                         Sequence 1, Application US/08076011
Patent No. 5521069
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 17041 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: ; LOCATION: ; LOCATION: ; LOCATION: US-08-076-011-1
                                                                                                                               RESULT 83
US-08-076-011-1/c
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RESULT

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Gaps

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COUNTRY:

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0.2%; Score 45; DB 3; Length 35060; 100.0%; Pred. No. 3.9e-08;
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: OTHER INFORMATION: /gene="AR"
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: NAME/KEY: exon
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: OTHER INFORMATION: /gene="ARS"
: OTHER INFORMATION: /number= 16
US-08-814-095-7
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FEATURE:
     LOCATION: complement (33779..33963)
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LOCATION: complement (32959..33094)
OCHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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IDENTIFICATION METHOD: experimental
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AMATION: /function= "arsenite resistance awation: gene"
                                                                                                                                                NAME/KEY: promoter LOCATION: 4089..22464 OTHER INFORMATION: /function= "ACHE Promotor" OTHER INFORMATION: /standard_name= "ACHE Promotor" FEATURE:
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LOCATION: 22465..2537
OTHER INFORMATION: /function= "non-translated"
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NAME/KEY: exon
LOCATION: 27255.28007
LOCATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 5
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LOCATION: complement (34092..34358)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
FEATURE:
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/number= 1
ANTI-SENSE: NO
ORIGIAML SOURCE:
ORGANISM: HOMO Sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: terminator
LOCATION: 27385.27387
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: terminator
LOCATION: 28129..28131
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: complement
OTHER INFORMATION: /
OTHER INFORMATION: /
OTHER INFORMATION: /
OTHER INFORMATION: /
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..264
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OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "Only one strand sequenced"
PUBLICATION INFORMATION:
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NAME/KEY: misc_feature
LOCATION: complement (220..238)
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OTHER INFORMATION: /standard_name= "PCR primer"
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OTHER INFORMATION: /citation= ([1])
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Weber, J. L. AUTHORS: May, P. E. AUTHORS: May, P. E. TITLE: Dinucleotide repeat polymorphism at the TITLE: D45171 locus
                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
RGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECHOME: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Cauca
TISSUE TYPE: Blood
IMMEDIATE SOURCE:
CLONE: Mfd22
POSITION IN GENOME:
CHOOMOSOME/SEGMENT: 4
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: repeat_region
LOCATION: 153..193
OTHER INFORMATION: /rpt_t;
OTHER INFORMATION: /rpt_f;
OTHER INFORMATION: /citat.
                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 264 Base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                         Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                               53717-1914
                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL:
                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-222-177A-10/c
; Sequence 10, Application US/08222177A
; Sequence 10, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; TITLE OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DeWitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
    Gaps
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                                                                                                                                                                                                                                                               APPLICANT: Fu. Ying-Hui
APPLICANT: Yu. Chang-En
APPLICANT: Oshima. Junko
APPLICANT: Muligan, John T.
APPLICANT: Muligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                               ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Le
3.5e-08;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INPORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 62-4900
TELEFAX: (206) 68-6031
INFORMATION FOR SEQ ID NO: 79:
                                                                                                                                                                                                Sequence 79, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-08-781-891-79
                                                                                                                                                                             US-08-781-891-79
Matches
                                                                                                                                                        RESULT
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94920
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: PER PROPRY disk
COMPUTER: PER PROPRY DISK
COMPUTER: PREAD PROPRY DISK
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
PRIOR APPLICATION DATA:
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APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Leuder, Leona L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.2%; Score 44; DB 2; Length 289;
100.0%; Pred. No. 1.6e-07;
ive 0; Mismatches 0; Indels
   Indels
                                                     ;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TILLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
IITLE OF INVENTION: MN Gene and Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D-0021.3D
                                                                                                                                                                                                                                       US-08-477-504A-63/c; Sequence 63, Application US/08477504A; Patent No. 5972353; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-486-756A-63/c
; Sequence 63, Application US/08486756A
Patent No. 5981711
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lander, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.2
Best Local Similarity 100.
Matches 44; Conservative
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   Matches
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR PATICATION: 424
PRIOR PATICATION: 424
PRIOR PATICATION: 1994
ATTORNEY/AGENT INFORMATION:
ANALY FOLGATION TO ATTORNEY TO ATTORNEY
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.2%; Score 44; DB 2; Length 289; 100.0%; Pred. No. 1.6e-07;
                                                                               AUTHORS: May, Paula E. TITLE: Abundant Class of Human DNA Polymorphisms TITLE: Which Can Be Typed Using the Polymerase Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.2%; Score 44; DB 1; L
100.0%; Pred. No. 1.6e-07;
ative 0; Mismatches 0;
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APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY, CACHELL TROUGH L. NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-481-658B-63/c
; Sequence 63, Application US/08481658B
2 Eatent No. 5955075
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                     AUTHORS: Weber, James L. AUTHORS: May, Paula E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                      PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415-435-0727
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Best Local Similarity
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Best Local Similarity
Matches 44; Conserv
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                                                                                                                                                                                 Reaction
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TELEFAX: 4
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US-08-481-658B-63
                                                                                                                                                                                                        JOURNAL:
VOLUME: 4
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,739
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy 10572 cctgccttggcctcccaaagtgctgggattacaggcgtgagcca 10615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0.08/477,504
FILING DATE: 0.7-UN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-UN-1994
ATTORNEY/AGENT INFORMATION:
REGISTATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEFNORE: 415-435-0727
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
TYPE: NUCLEIC CARROLLING:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
TYPE: NUCLEIC CARROLLING:
STRANDENESS: SINGLE
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STREET: 369 Pine Street, Suite 610
                                                                                                                                                                                                                                                                                                    D-0021.3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 08/485,862
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-787-739-63/c; Sequence 63, Application US/08787739 Patent No. 6027887; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-08-485-862B-63
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07-JUN-1995
FILING DATE: 07-JUN-1995
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.2%; Score 44; DB 2; L. Best Local Similarity 100.0%; Pred. No. 1.6e-07; Matches 44; Conservative 0; Mismatches 0;
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Patent No. 598938
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Frotein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 63: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                   ADDRESSEE: Leona L. Laud
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 289 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
      NUMBER OF SEQUENCES: 86
                                        CORRESPONDENCE ADDRESS:
                                                                                              STREET: 6 Mariposa
CITY: Tiburon
STATE: California
COUNTRY: USA
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STATE: California
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US-08-485-862B-63/c
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Gaps
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ZIP: 94920

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IMP PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,863A

FILING DATE: 07-JUN-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.

REGISTRATION NUMBER: D-0021.3G

REFERENCE/POCKET NUMBER: D-0021.3G

TELECOMMUNICATION INFORMATION:

TELECOMMUNICA
                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 289;
1.6e-07;
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100.0%; Pred. No. 1.6e-07;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: Gariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                              Query Match 0.2%; Score 44; DB Best Local Similarity 100.0%; Pred. No. 1.6 Matches 44; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 94
US-00-485-863A-63/c
; Sequence 63, Application US/08485863A
; Patent No. 6093548
                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                   289 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 289 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.0
Matches 44; Conservative
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                                                                                                                                                                                                                                   ; ANTI-SENSE:
US-08-487-077A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE:
US-08-485-863A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,077A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-0814 87-0778-63/C
Sequence 63, Application US/08487077A
Sequence 63, Application US/08487077A
Sequence 63, Application US/08487077A
Sequence 63, Application US/08487077A
Setent No. 6059242
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESSORE: Leona L. Lauder
STREET: 6 Mariposa Court
STREET: 6 Mariposa Court
STREET: 6 California
COUMTRY: USA
ZIP: 94920
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATE: 07-JUN-1995
PRIOR APPLICATION DATE: 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY.AGENT INFORMATION:
NAME: LAUGEY.LEONA L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.4
TELEPHONE: 415-981-2034
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
LENGTH: 289 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
FILING DATE: D7-JUN-1994
PRIOR APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION: NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy 10572 cctgccttggcctcccaaagtgctgggattacaggcgtgagcca 10615
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILLING DATE: 07-JUN-1995
CLASSIFICATION: 4.24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 CCTGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCA 221
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100.0%; Pred. No. 1.3e-07;
tive 0; Mismatches 0;
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Patent No. 5972353
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
ITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
DESCRIPTION: 6th MN intron
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STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 44
SEQUENCE CHARACTERISTICS:
LENGTH: 1334 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 100.(
Matches 44; Conservative
                                                                                                                                     COMPUTER READABLE FORM:
                                    California
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N
   Tiburon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE:
US-08-481-658B-44
                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATE: PC-DOS/MS-DOS
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/485,049D
FILING DATE: 07-JUN-1995
RIOR APPLICATION: 435
RIOR APPLICATION: TO A A STANDARD APPLICATION: TO A STANDARD APPLICATION TO A STANDARD A STANDARD APPLICATION TO A STANDARD A STANDARD
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56 CCTGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCA 13
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100.0%; Pred. No. 1.6e-07;
tive 0; Mismatches 0;
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Patent No. 5955075
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 6 Mariposa Court
                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFCATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY AGENT INFORMATION:
NAME: LAUGET, LEONA L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELEPHONE: 415-981-2034
TELEPHONE: 415-981-0332
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LBNGTH : 289 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                              US-08-485-049D-63/c
; Sequence 63, Application US/08485049D
; Patent No. 6204370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS AND
CURRENM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
COUNTRY: USA
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Best Local Similarity
Matches 44; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                 0.2%; Score 44; DB 2; Length 1334;
100.0%; Pred. No. 1.3e-07;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION UNMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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100.0%; Pred. No. 1.3e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D-0021.3D
                                                                                                                                                                                                                                                                                                                                                                                Sequence 44, Application US/08485862B Patent No. 5989838 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REPERENCE/DOCKET NUMBER: D-0(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-034
TELEFAX: 415-435-0727
  6th MN intron
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) DESCRIPTION: 6th MN intron HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 44: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1334 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                 Query Match 0.2%
Best Local Similarity 100.0
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.2°
Best Local Similarity 100.
Matches 44; Conservative
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  DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                         RESULT 99
US-08-485-862B-44/C
                    HYPOTHETICAL:
HYPOTHETICAL:
ANTI-SENSE:
US-08-486-756A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE:
US-08-485-862B-44
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING STERM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY AMPRORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy 10572 cctgccttggcctcccaaagtgctgggattacaggcgtgagcca 10615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 CCTGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCA 221
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Sequence 44, Application US/08486756A
Sequence 44, Application US/08486756A
Selent No. 5981711
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION:
TELEPHONE: 415-435-2034
                                                                                         D-0021.3D
                                       NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFRERENCE/DOCKET NUMBER: D-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1334 base pairs
ITYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
DESCRIPTION: 6th MN intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-435-0727 INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE; DNA (genomic)
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1334 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 44; Conserva
                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE: NO US-08-477-504A-44
                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94920
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g

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RESULT 100

Sequence 44,0 Application US/0878739

Sequence 44,0 Application US/0878739

Response 44,0 Application US/0878739

Response 42,0 Application US/0878739

Response 42,0 Application US/0878739

APPLICANT: PASTOCHE, Janomit Comparing September Engles 23,0 Float Structure Comparing September Engles 23,0 Float Structure Comparing September Engles 24,0 Application OWNER; USA DEPLICANTION DATA:

COUNTRY: USA DEPLICANTION DATA:

COUNTRY: USA DEPLICANTION DATA:

RESIDENCE APPLICANTION DATA:

APPLICANTION NUMBER: US 08,445,049

PRIOR APPLICANTION NUMBER: US 08,445,649

PRIOR APPLICANTION NUMBER: US 08,445,663

PRIOR APPLICANTION NUMBER: US 08,445,677

PRESENCE/CORFEE UNBERS: US 09,437

PRODUCCT: LIGHT OF US SED 10 WAI APPLICANTION NUMBER: US 08,447

PRODUCCT: LIGHT OF US SED 10 WAI APPLICANTION NUMBER: US 08,447

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PRODUCCT: LIGHT OF US SED 10 WAI APPLICANTION NUM
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Db 264 CCTGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCA 221
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Search completed: November 3, 2001, 00:58:55 Job time: 99845 sec

Query Match 0.2%; Score 44; DB 3; Length 1334;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 10572 cctgccttggcctcccaaagtgctgggattacaggcgtgagcca 10615